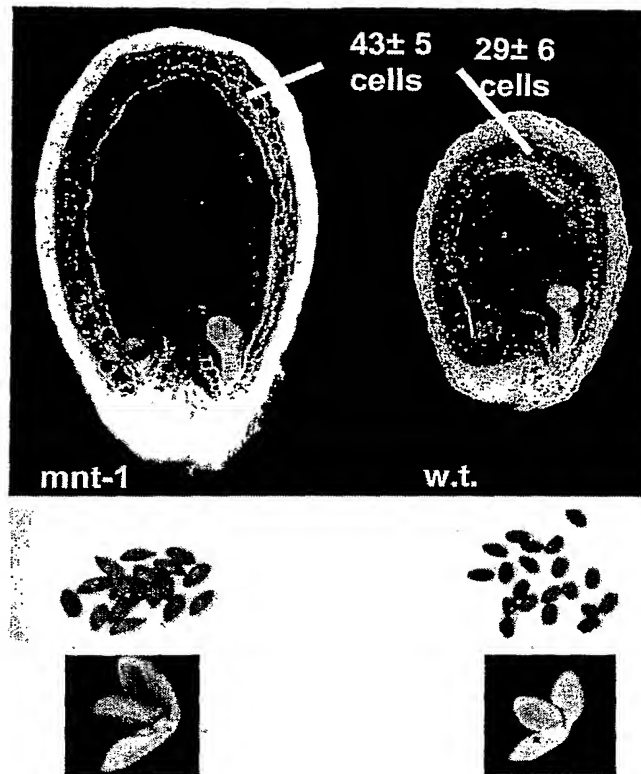


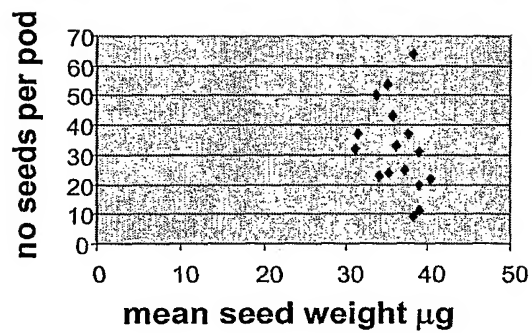
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# Figure 1

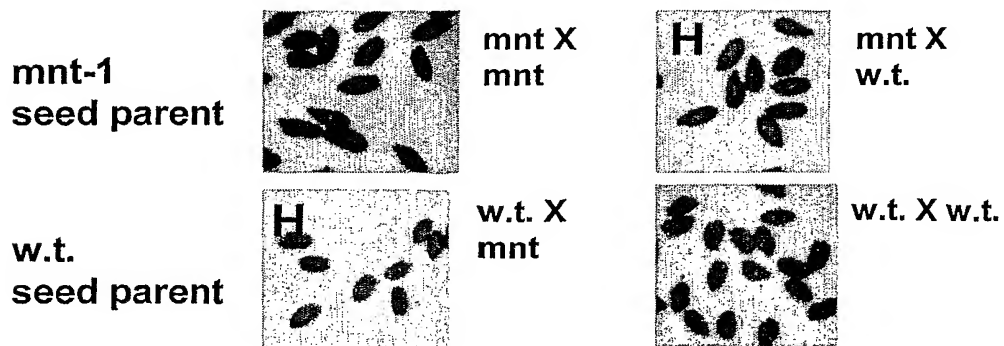
## 1A mnt-1 vs wild-type seeds



## 1B Seed weight vs no. seeds per pod in mnt-1

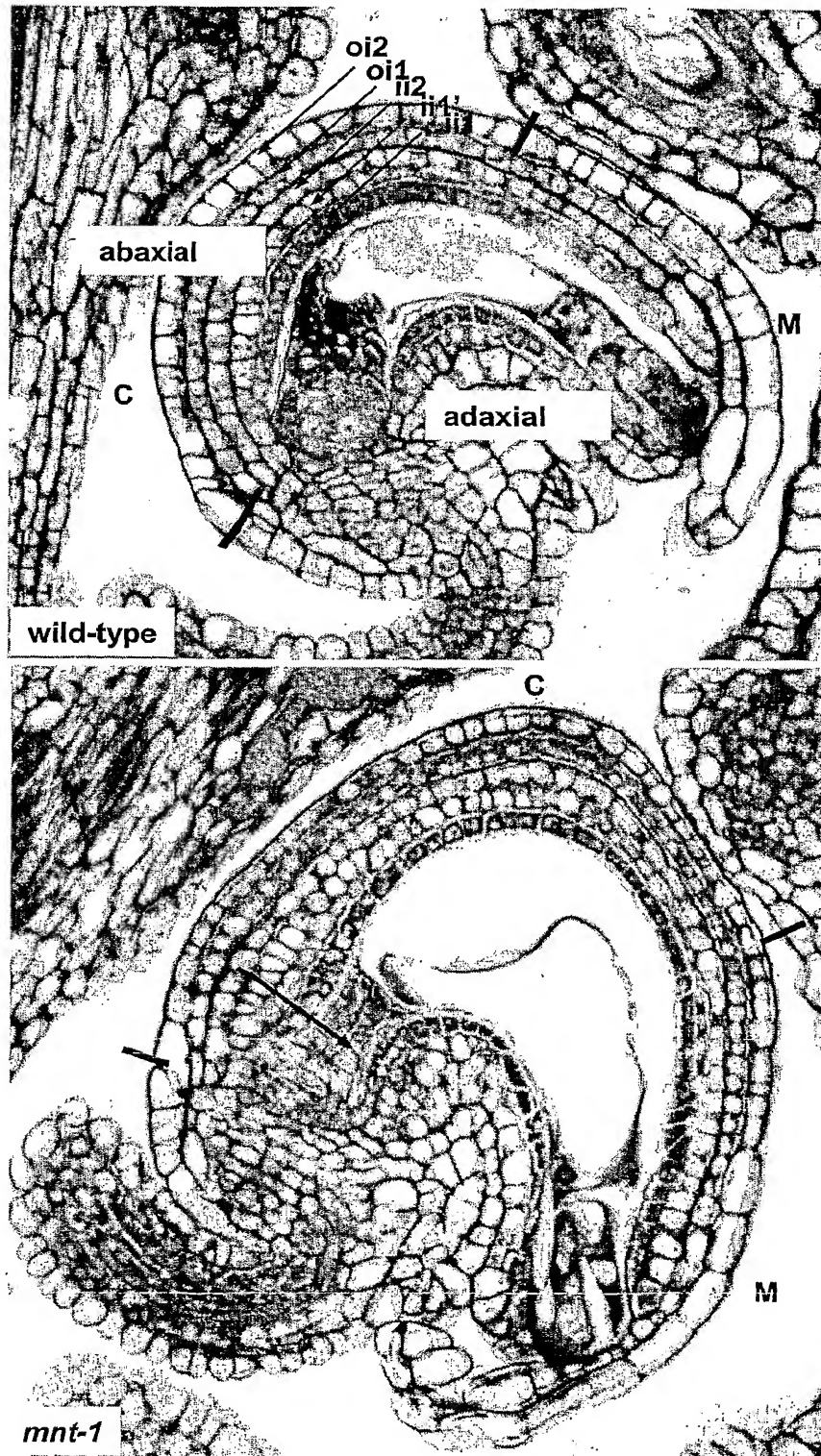


## 1C Maternal effect of mnt-1 mutation

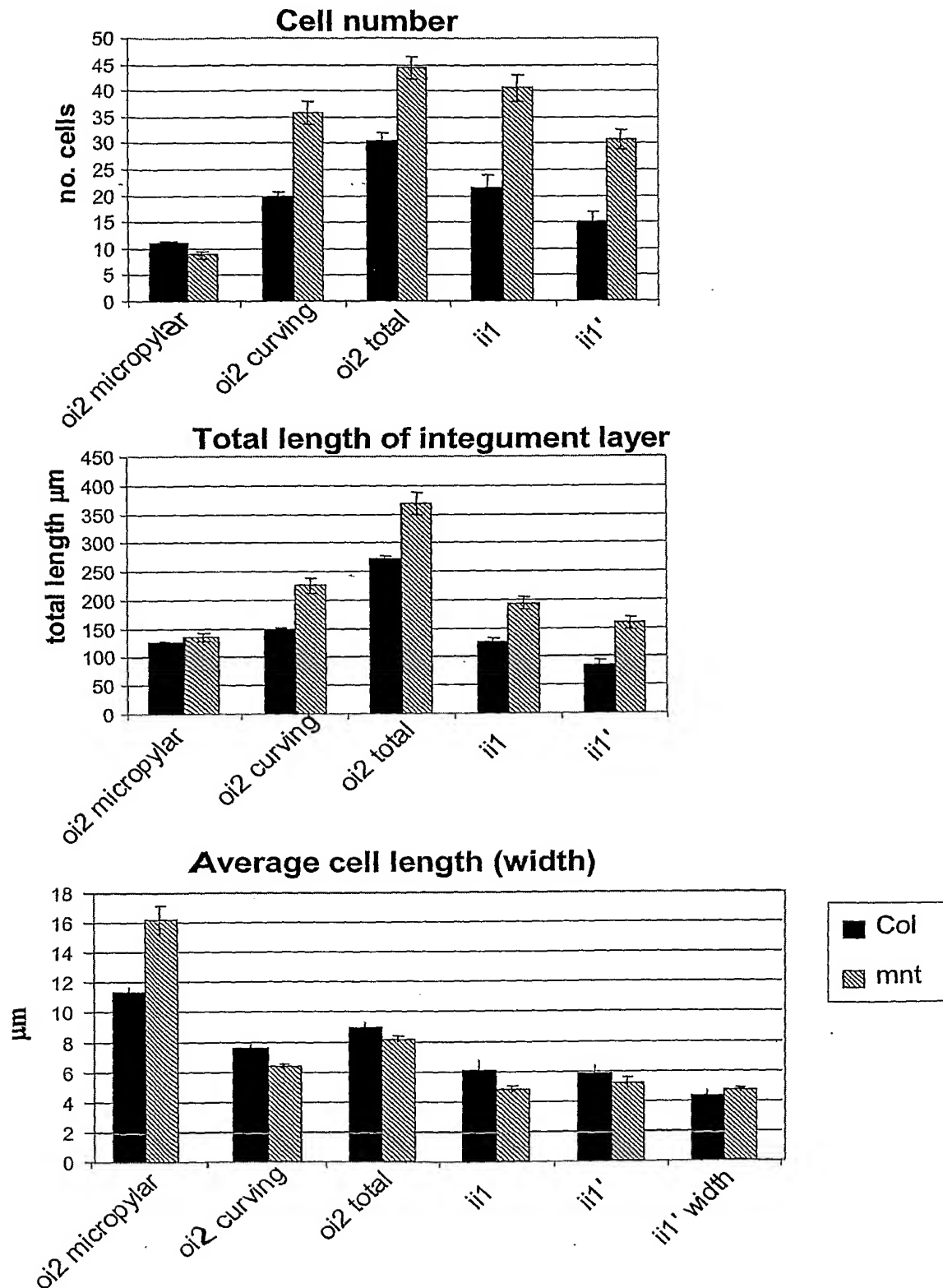


## Figure 2

### 2A Mature w.t. and *mnt-1* ovules



## 2B Cell number and size in w.t. and *mnt-1* integuments

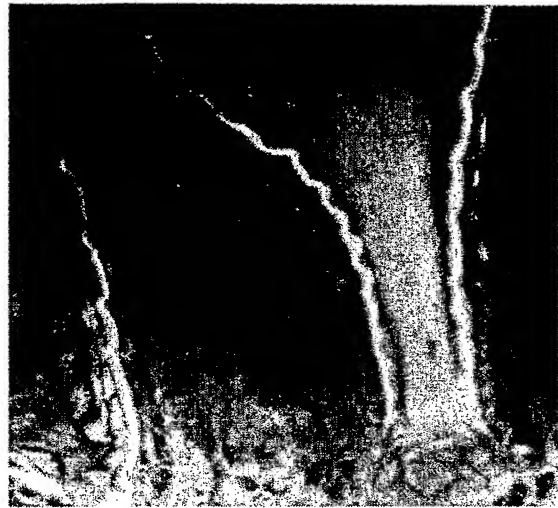


# **Figure 3**

## **Chalazal endosperm**



**w.t. 7DAP**



**mnt-1 7DAP**



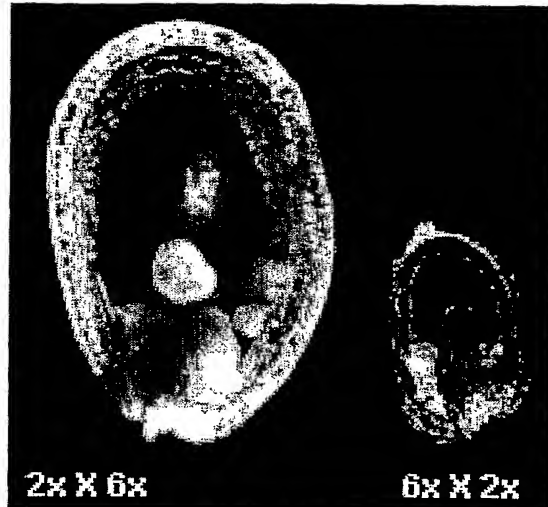
**2x X 6x 5 DAP**

**Bars = 50  $\mu$ m**



# Figure 4

## 4A Endosperm-led growth



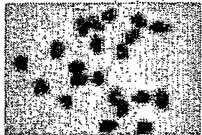
big cavity

normal

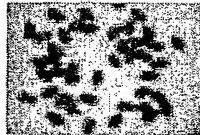
small



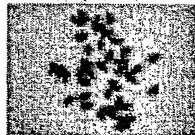
C24 2x X 4x



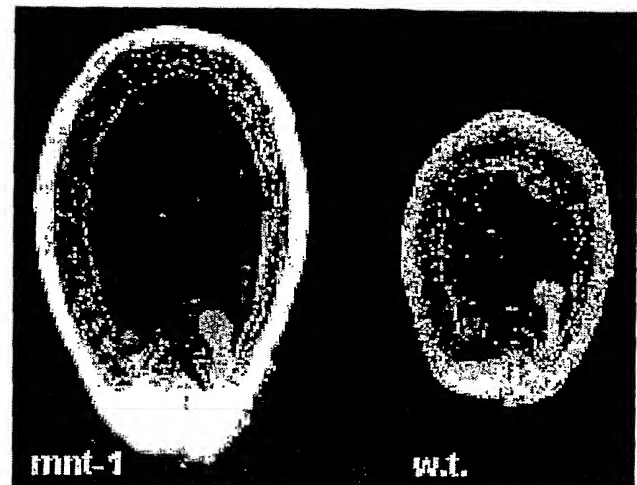
2x X 2x



4x X 2x



## 4B Integument-led growth



big cavity

normal



Col mnt-1



Col w.t.



## 4C 'Big bag' hypothesis: seed and embryo size set by size of the seed cavity

1. Division in endosperm  
(maternal and paternal control)
2. Division in integuments/  
seed coat (maternal control)



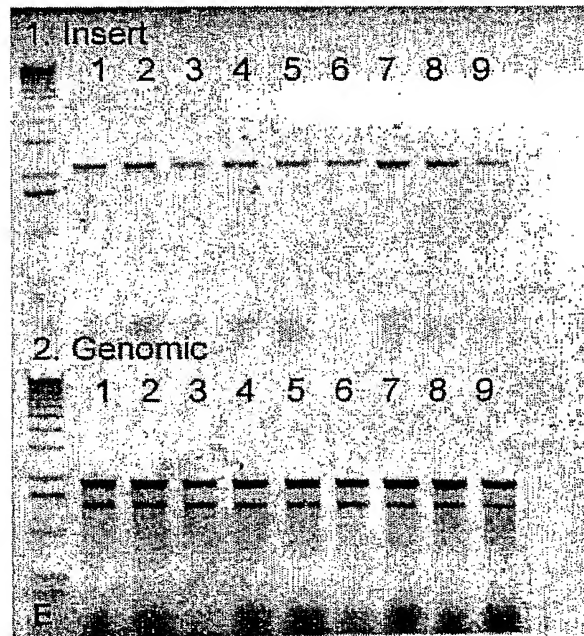
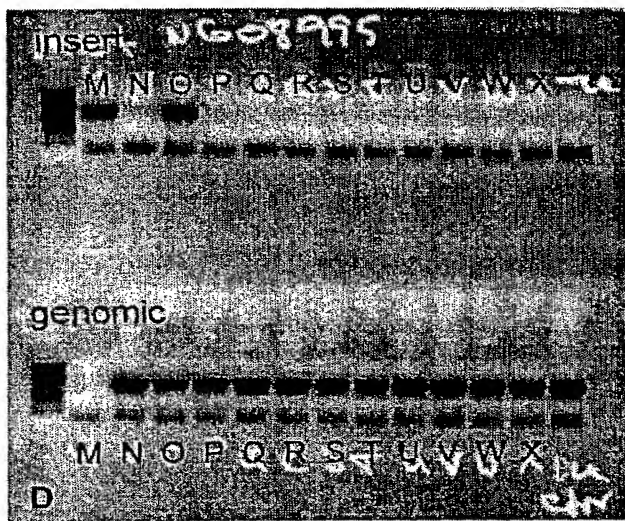
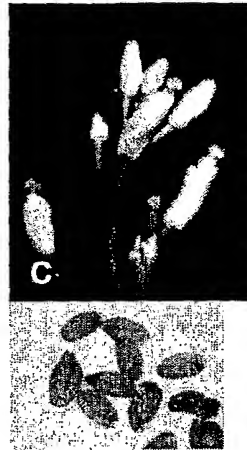
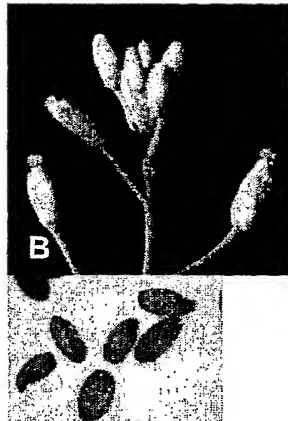
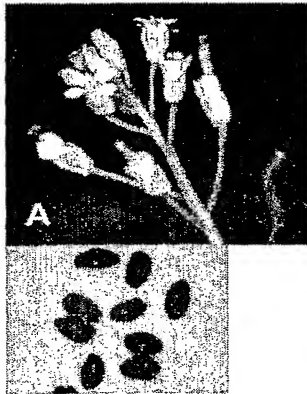
## Figure 5

### Allelism of mnt-1 and Salk insertion line 108995

Col-3 w.t.

mnt-1

Salk 108995 homozygote



F1 mnt-1 X Salk 108995



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# Figure 6

## Alignment of w.t. MNT and mutant mnt-1 cDNA

MNT                   \*                   20                   \*                   40                   \*                   60

ATGGCGAGTTGGGAGGTTTCAATGAAAGGTAATCGTGGAGGAGATAACTTCTCCTCCTCT

ATGGCGAGTTGGGAGGTTTCAATGAAAGGTAATCGTGGAGGAGATAACTTCTCCTCCTCT

mnt-1

                 \*                   80                   \*                   100                   \*                   120

GGTTTTAGTGACCCTAAGGAGACTAGAAATGTCTCCGTCGCCGGCGAGGGGCAAAAAGT

GGTTTTAGTGACCCTAAGGAGACTAGAAATGTCTCCGTCGCCGGCGAGGGGCAAAAAGT

                 \*                   140                   \*                   160                   \*                   180

AATTCTACCCGATCCGCTGCGGCTGAGCGTGCTTTGGACCCTGAGGCTGCTCTTTACAGA

AATTCTACCCGATCCGCTGCGGCTGAGCGTGCTTTGGACCCTGAGGCTGCTCTTTACAGA

                 \*                   200                   \*                   220                   \*                   240

GAGCTATGGCAGGCTTGTGCTGGTCCGCTTGTGACGGTTCTAGACAAGACGACCGAGTC

GAGCTATGGCAGGCTTGTGCTGGTCCGCTTGTGACGGTTCTAGACAAGACGACCGAGTC

                 \*                   260                   \*                   280                   \*                   300

TTCTATTTTCTCCTCAAGGACACATCGAGCAGGTGGAGGCTTCGACGAACCAGGCGGCAGAA

TTCTATTTTCTCCTCAAGGACACATCGAGCAGGTGGAGGCTTCGACGAACCAGGCGGCAGAA

                 \*                   320                   \*                   340                   \*                   360

CAACAGATGCCTCTCTATGATCTTCCGTCAAAGCTTCTCTGTCCAGTTATTAATGTAGAT

CAACAGATGCCTCTCTATGATCTTCCGTCAAAGCTTCTCTGTCCAGTTATTAATGTAGAT

                 \*                   380                   \*                   400                   \*                   420

TTAAAGGCAGAGGCAGATACAGATGAAGTTTATGCGCAGATTACTCTTCTTCTCCTGAGGCT

TTAAAG-----AGGCAGATACAGATGAAGTTTATGCGCAGATTACTCTTCTTCTCCTGAGGCT

                 \*                   440                   \*                   460                   \*                   480

AATCAAGACGAGAATGCAATTGAGAAAGAAGCGCCTCTTCCCTCCACCTCCGAGGTTCCAG

AATCAAGACGAGAATGCAATTGAGAAAGAAGCGCCTCTTCCCTCCACCTCCGAGGTTCCAG

                 \*                   500                   \*                   520                   \*                   540

GTGCATTCTTTCTGCAAAACCTTGACTGCATCCGACACAACTACACATGGTGGATTTTCT

GTGCATTCTTTCTGCAAAACCTTGACTGCATCCGACACAACTACACATGGTGGATTTTCT

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\* 560 \* 580 \* 600  
GTTCTTAGGCGACATGCGGATGAATGTCTCCACCTCTGGATATGTCTCGACAGCCTCCC  
GTTCTTAGGCGACATGCGGATGAATGTCTCCACCTCTGGATATGTCTCGACAGCCTCCC

\* 620 \* 640 \* 660  
ACTCAAGAGTTAGTTGCAAAGGATTTGCATGCAAATGAGTGGCGATTTCAGACATATATTC  
ACTCAAGAGTTAGTTGCAAAGGATTTGCATGCAAATGAGTGGCGATTTCAGACATATATTC

\* 680 \* 700 \* 720  
CGGGGTCAACCACGGAGGCATTTGCTACAGAGTGGGTGGAGTGTGTTTGTTAGCTCCAAA  
CGGGGTCAACCACGGAGGCATTTGCTACAGAGTGGGTGGAGTGTGTTTGTTAGCTCCAAA

\* 740 \* 760 \* 780  
AGGCTAGTTGCAGGCGATGCGTTTATATTTCTAAGGGGCGAGAATGGAGAATTAAGAGTT  
AGGCTAGTTGCAGGCGATGCGTTTATATTTCTAAGGGGCGAGAATGGAGAATTAAGAGTT

\* 800 \* 820 \* 840  
GGTGTAAAGGCGTGCGATGCCACAACAAGGAAACGTGCCGTCTTCTGTTATATCTAGCCAT  
GGTGTAAAGGCGTGCGATGCCACAACAAGGAAACGTGCCGTCTTCTGTTATATCTAGCCAT

\* 860 \* 880 \* 900  
AGCATGCATCTTGGAGTACTGGCCACCGCATGGCATGCCATTTCAACAGGGACTATGTTT  
AGCATGCATCTTGGAGTACTGGCCACCGCATGGCATGCCATTTCAACAGGGACTATGTTT

\* 920 \* 940 \* 960  
ACAGTCTACTACAAACCCAGGACGAGCCCATCTGAGTTTATTGTTCCGTTTCGATCAGTAT  
ACAGTCTACTACAAACCCAGGACGAGCCCATCTGAGTTTATTGTTCCGTTTCGATCAGTAT

\* 980 \* 1000 \* 1020  
ATGGAGTCTGTTAAGAATAACTACTCTATTGGCATGAGATTCAAAATGAGATTTGAAGGC  
ATGGAGTCTGTTAAGAATAACTACTCTATTGGCATGAGATTCAAAATGAGATTTGAAGGC

\* 1040 \* 1060 \* 1080  
GAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGAGTCTGATCCT  
GAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGAGTCTGATCCT

\* 1100 \* 1120 \* 1140  
ACTAGGTGGCCAAAATCAAAGTGGAGATCCCTCAAGGTGAGATGGGATGAGACTTCTAGT  
ACTAGGTGGCCAAAATCAAAGTGGAGATCCCTCAAGGTGAGATGGGATGAGACTTCTAGT

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\* 1160 \* 1180 \* 1200  
ATTCTCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCTCCTGCT  
ATTCTCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCTCCTGCT

\* 1220 \* 1240 \* 1260  
TTGAGTCCTGTTCCAATGCCTAGGCCTAAGAGGCCAGATCAAATATAGCACCTTCATCT  
TTGAGTCCTGTTCCAATGCCTAGGCCTAAGAGGCCAGATCAAATATAGCACCTTCATCT

\* 1280 \* 1300 \* 1320  
CCTGACTCTTCGATGCTTACCAGAGAAGGTACAACCTAAGGCAAACATGGACCCCTTTACCA  
CCTGACTCTTCGATGCTTACCAGAGAAGGTACAACCTAAGGCAAACATGGACCCCTTTACCA

\* 1340 \* 1360 \* 1380  
GCAAGCGGACTTTCAAGGGTCTTGCAAGGTCAAGAATACTCGACCTTGAGGACGAAACAT  
GCAAGCGGACTTTCAAGGGTCTTGCAAGGTCAAGAATACTCGACCTTGAGGACGAAACAT

\* 1400 \* 1420 \* 1440  
ACTGAGAGTGTAGAGTGTGATGCTCCTGAGAATTCTGTTGCTCTGGCAATCTTCAGCGGAT  
ACTGAGAGTGTAGAGTGTGATGCTCCTGAGAATTCTGTTGCTCTGGCAATCTTCAGCGGAT

\* 1460 \* 1480 \* 1500  
GATGATAAGGTTGACGTGGTTTCGGGTTCTAGAAAGATATGGATCTGAGAACTGGATGTCC  
GATGATAAGGTTGACGTGGTTTCGGGTTCTAGAAAGATATGGATCTGAGAACTGGATGTCC

\* 1520 \* 1540 \* 1560  
TCAGCCAGGCATGAACCTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAACATAGAT  
TCAGCCAGGCATGAACCTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAACATAGAT

\* 1580 \* 1600 \* 1620  
CCATCCCATGGTCAGCGGATACCTTTTTATGACCATTTCATCATCACCTTCTATGCCTGCA  
CCATCCCATGGTCAGCGGATACCTTTTTATGACCATTTCATCATCACCTTCTATGCCTGCA

\* 1640 \* 1660 \* 1680  
AAGAGAACTCTTGAGTGATTTCAGAAAGCAAGTTCGATTATCTTGCTAACCAGTGGCAGATG  
AAGAGAACTCTTGAGTGATTTCAGAAAGCAAGTTCGATTATCTTGCTAACCAGTGGCAGATG

\* 1700 \* 1720 \* 1740  
ATACACTCTGGTCTCTCCCTGAAGTTACATGAATCTCCTAAGGTACCTGCAGCAACTGAT  
ATACACTCTGGTCTCTCCCTGAAGTTACATGAATCTCCTAAGGTACCTGCAGCAACTGAT



\* 1760 \* 1780 \* 1800  
GCGTCTCTCCAAGGGCGATGCAATGTTAAATACAGCGAATATCCTGTTCTTAATGGTCTA  
GCGTCTCTCCAAGGGCGATGCAATGTTAAATACAGCGAATATCCTGTTCTTAATGGTCTA

\* 1820 \* 1840 \* 1860  
TCGACTGAGAATGCTGGTGGTAACTGGCCAATACGTCCACGTGCTTTGAATTATTATGAG  
TCGACTGAGAATGCTGGTGGTAACTGGCCAATACGTCCACGTGCTTTGAATTATTATGAG

\* 1880 \* 1900 \* 1920  
GAAGTGGTCAATGCTCAAGCGCAAGCTCAGGCTAGGGAGCAAGTAACAAAACAACCCTTC  
GAAGTGGTCAATGCTCAAGCGCAAGCTCAGGCTAGGGAGCAAGTAACAAAACAACCCTTC

\* 1940 \* 1960 \* 1980  
ACGATACAAGAGGAGACAGCAAAGTCAAGAGAAGGGAACTGCAGGCTCTTTGGCATTTCCT  
ACGATACAAGAGGAGACAGCAAAGTCAAGAGAAGGGAACTGCAGGCTCTTTGGCATTTCCT

\* 2000 \* 2020 \* 2040  
CTGACCAACAACATGAATGGGACAGACTCAACCATGTCTCAGAGAAACAACCTTGAATGAT  
CTGACCAACAACATGAATGGGACAGACTCAACCATGTCTCAGAGAAACAACCTTGAATGAT

\* 2060 \* 2080 \* 2100  
GCTGCGGGGCTTACACAGATAGCATCACCAAAGGTTGAGGACCTTTGAGATCAGTCAAAA  
GCTGCGGGGCTTACACAGATAGCATCACCAAAGGTTGAGGACCTTTGAGATCAGTCAAAA

\* 2120 \* 2140 \* 2160  
GGGTCAAATCAACAAACGATCATCGTGAACAGGGGAAGACCATTCCAGACTAATAATCCT  
GGGTCAAATCAACAAACGATCATCGTGAACAGGGGAAGACCATTCCAGACTAATAATCCT

\* 2180 \* 2200 \* 2220  
CATCCGAAGGATGCTCAAACGAAAACCAACTCAAGTAGGAGTTGCACAAAGGTTCAACAAG  
CATCCGAAGGATGCTCAAACGAAAACCAACTCAAGTAGGAGTTGCACAAAGGTTCAACAAG

\* 2240 \* 2260 \* 2280  
CAGGGAATTGCACCTTGGCCGTTGAGTGGATCTTTCAAAGTTCCAAAACCTATGAGGAGTTA  
CAGGGAATTGCACCTTGGCCGTTGAGTGGATCTTTCAAAGTTCCAAAACCTATGAGGAGTTA

\* 2300 \* 2320 \* 2340  
GTCGCTGAGCTGGACAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTAAGAAAGAT  
GTCGCTGAGCTGGACAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTAAGAAAGAT

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\* 2360 \* 2380 \* 2400  
TGGTTGATAGTTTACACAGATGAAGAGAATGATATGATGCTTGTTGGTGACGATCCTTGG  
TGGTTGATAGTTTACACAGATGAAGAGAATGATATGATGCTTGTTGGTGACGATCCTTGG

\* 2420 \* 2440 \* 2460  
CAGGAGTTTTGTTGCATGGTTCGCAAAATCTTCATATACACGAAAGAGGAAGTGAGGAAG  
CAGGAGTTTTGTTGCATGGTTCGCAAAATCTTCATATACACGAAAGAGGAAGTGAGGAAG

\* 2480 \* 2500 \* 2520  
ATGAACCCGGGGACTTTAAGCTGTAGGAGCGAGGAAGAAGCAGTTGTTGGGGAAGGATCA  
ATGAACCCGGGGACTTTAAGCTGTAGGAGCGAGGAAGAAGCAGTTGTTGGGGAAGGATCA

\* 2540 \* 2560 \* 2580  
GATGCAAAGGACGCCAAGTCTGCATCAAATCCTTCATTGTCCAGCGCTGGGAACTCTTAA  
GATGCAAAGGACGCCAAGTCTGCATCAAATCCTTCATTGTCCAGCGCTGGGAACTCTTAA



# Figure 7

## Alignment of w.t. MNT and mutant mnt-1 protein

MNT	*	20	*	40	*	60
MASSEVSMKGNRGGDNFSSSGFSDPKETRNVSVAGEGOKSNSTRSAAAERALDPEAALYR						
MASSEVSMKGNRGGDNFSSSGFSDPKETRNVSVAGEGOKSNSTRSAAAERALDPEAALYR						
mnt-1						
	*	80	*	100	*	120
ELWHACAGPLVTVPQODDRVFYFPQGHIEQVEASTNQAAEQCOMPLYDLP SKLLCRVINVD						
ELWHACAGPLVTVPQODDRVFYFPQGHIEQVEASTNQAAEQCOMPLYDLP SKLLCRVINVD						
	*	140	*	160	*	180
LKAEADTDEVYAOITLLPEANQDENATEKEAPLPPPPRFQVHSFCKTLTASDTSTHGGS						
LKRQIQMKFMRRLLEFLRLIKTRMQLRKKRLFLHLRGSRCIRSAKP-----						
	*	200	*	220	*	240
VLRRHADECLPPLDMSRQPPTQELVAKDLHANEWRFRTFRGQPRRHLLQSGWSVFVSSK						
-----						
	*	260	*	280	*	300
RLVAGDAFIFLRGENGELRVGVRRAMRQQGNVPSSVISSSHMHGLGVLATAWHAISTGTME						
-----						
	*	320	*	340	*	360
TVYYKPTSPSEFIVPFDOYMESVKNNYSIGMRFKMRFEGEREAPQRTGTIVGLEESDP						
-----						
	*	380	*	400	*	420
TRWPKSKWRSCLKVRWDETSSIPRPDRVSPWKVEPALAPPALSPVPMRPKRPRSNIPSS						
-----						
	*	440	*	460	*	480
PDSSMLTREGTTKANMDPLPASGLSRVLOGQEYSTLRTHKTESVECDAPENSVVWQSSAD						
-----						
	*	500	*	520	*	540
DDKVDVVSQSRRYGSENMSSARHEPTYDLLSGFGTNIDPSHGQRIPEYDHSSSPSMPA						
-----						
	*	560	*	580	*	600
KRILSDSEGKFDYLANQWQMIHSGLSLKLHESPKVPAATDASLQGRCNVKYSEYPVLNGL						
-----						

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\* 620 \* 640 \* 660  
STENAGGNWP IRPRALNYYEEVVNAQAAQAREQVTKQPF TIOEETAKSREGNCRLEGIP

---

\* 680 \* 700 \* 720  
LTNNMNGTDSTMSQRNNLNDAGLTQTASPKVQDLSDQSKGSKSTNDHREQGRPFQTNNP

---

\* 740 \* 760 \* 780  
HPKDAQT KTNSSRSCTKVHKOGIALGRSVDLSKFQNYEELVAELDRLEFNGELMAPKKD

---

\* 800 \* 820 \* 840  
WLIIVYTDEENDMMLVGDDPWQEFFCCMVRKIFIYTKEEVRKMNPGLSCRSEEEAVVGEFS

---

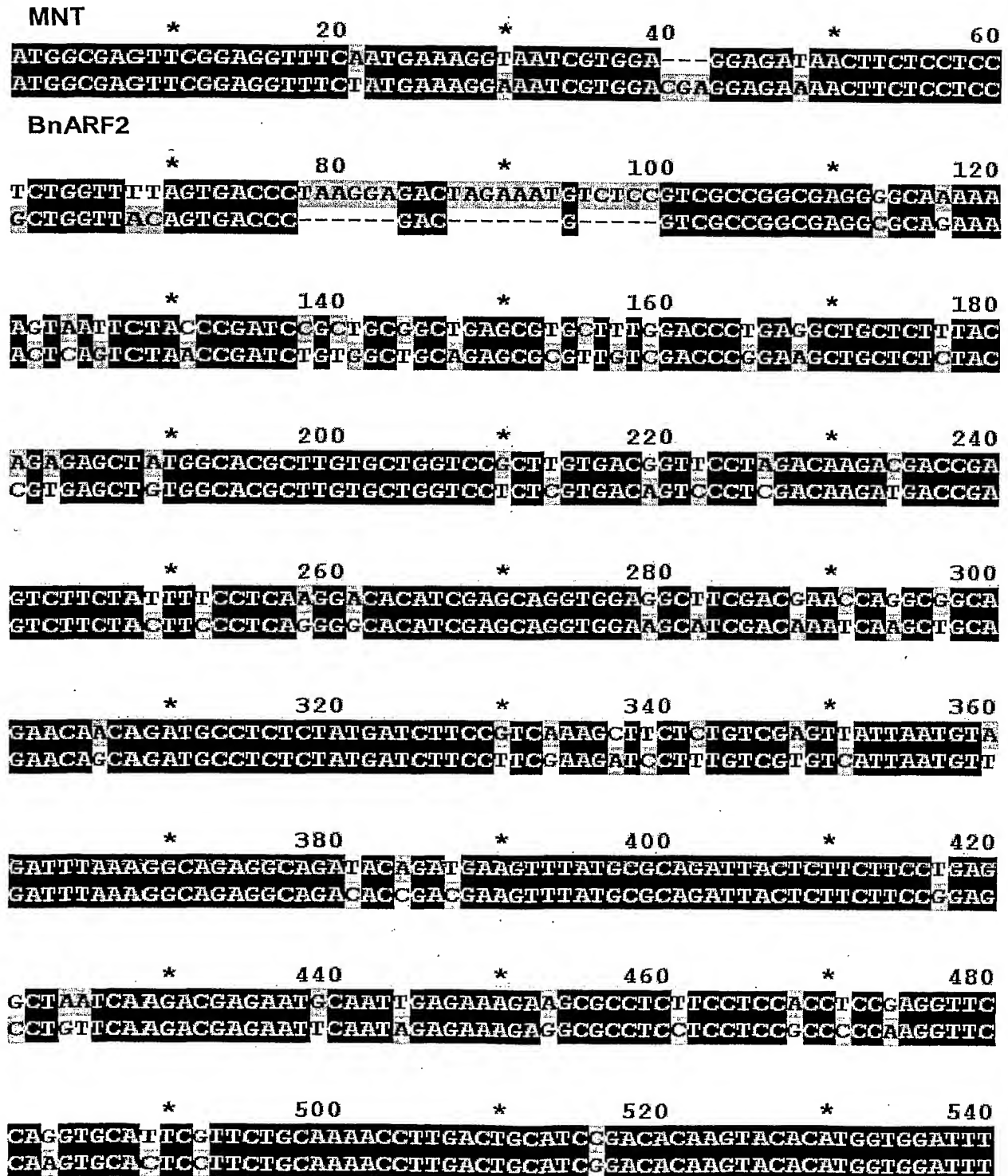
\*  
DAKDAKSASNPSLS SAGNS

---

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# Figure 8

## Alignment of MNT and BnARF2 cDNA



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\* 560 \* 580 \* 600  
TCTGTTCTTAGGCGACATGCGGATGAATGTCTCCACCTCTGGATATGTCTCGACAGCCT  
TCTGTGCTTAGGCGGACATGCGGATGAATGTCTCCACCTCTGGATATGTCTACGTCACACCT

\* 620 \* 640 \* 660  
CCCACTCAAGAGTTAGTTGCAAAGGATTGTCATGCAAATGAGTGGCGATTTCAGACATATA  
CCTACTCAGGAGTTAGTTGCAAAGGATGTCATGCAAGCGAGTGGCGTTTCGACATATT

\* 680 \* 700 \* 720  
TTCCGGGGTCAACCACGGAGGCATTTGCTACAGAGTGGGTGGAGTGTGTTTGTTAGCTCC  
TTCCGGGGTCAACCACGGAGGCATTTGCTTCAGAGTGGATGGAGCGTGTGTTGTAGCTCC

\* 740 \* 760 \* 780  
AAAGGGCTAGTTGCAGGCGATGCGTTTATATTTCTAAGGGGCGAGAATGGAGAATTAAAGA  
AAGAGGGCTGTTGCAGGCGATGCTTTTATATTTCTAAGGGGCGAGAATGGAGAATTACST

\* 800 \* 820 \* 840  
GTGGTGTAAAGGCGTGCGATGCGACAAACAAAGGAAACGTGCCGTCTTCTGTTATATCTAGC  
GTGGTGTAAAGGCGTGCAATGCGGCAGCAAGGAAATGTGCCATCCCTCTGTTATATCAAGC

\* 860 \* 880 \* 900  
CATAGCATGCATCTTGGAGTACTGGCCACCGCATGGCATGCCATTTCACACGGGACTATG  
CACAGCATGCATCTCGGAGTATTGGCCACTGCCCTGGCACGCTATTTCACACTGGAACCATG

\* 920 \* 940 \* 960  
TTTACAGTCTACTACAAACCAGGACGAGGCCATCTGAGTTTATTGTTCCGTTTGATCAG  
TTTACAGTCTACTATAAACCAGGACTAGTCCTTCAGAGTTTATTGTTCCGTTTGATCAG

\* 980 \* 1000 \* 1020  
TATATGGAGTCTGTAAAGAATAACTACTCTATTGGCATGAGATTCAAAATGAGATTTGAA  
TATACGGAGTCCGTGAAGATAACTACTCCATAGGCATGAGATTTAAATGAGATTTGAA

\* 1040 \* 1060 \* 1080  
GGCGAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGAGTCTGAT  
GGCGAAGAGGCTCCGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGACTCTGAC

\* 1100 \* 1120 \* 1140  
CCTACTAGGTGGCCAAATCAAAATGGAGATCCCTCAAGGTGAGATGGGATGAGACTTCT  
CCACAGAGGTGGCCAAATCAAAATGGAGATCCCTCAAGGTACGGTGGGATGAGACCACT

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\* 1160 \* 1180 \* 1200  
AGTATTCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCTCCT  
AGTATTCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCTCCT

\* 1220 \* 1240 \* 1260  
GCTTTGAGTCCTGTCCCAATGCCTAGGCCTAAGAGGCCAGATCAAATATAGCAGCTTCA  
GCTTTGAGTCCTGTCCCAATGCCTAGGCCTAAGAGGCCAGATCTAATCTAGCTTCTTCA

\* 1280 \* 1300 \* 1320  
TCTCCTGACTCTTCGATGCTTACCAGAGAAGGTACAACTAAGGCCAAACATGGACCCTTTA  
ACTCCGGACTCTTCGATGCTTACCAGAGAAGGTACAACTAAGGCCAAACATGGACCCTTTA

\* 1340 \* 1360 \* 1380  
CCAGCAAGCGGACTTTCAGGGTCTTGCAAGGTCAAGAATACTCGACCTTGAGGACGAAA  
CCGGCAAGTGGACTATCAAGGGTCTTGCAAGGTCAAGAATACTCGACCTTGAGGACGAAA

\* 1400 \* 1420 \* 1440  
CATACTGAGAGTGTAGAGTGTGATGCTCCTGAGAAATTCCTGTTGTCTGGCAATCTTCAGCG  
CATGTTGAGAGTGTAGAAATGCGATGCTCCTGAGAAATTCCTGTTGTCTGGCAATCTTCAGCT

\* 1460 \* 1480 \* 1500  
GATGATGATAAGGTTGACGTGCTTTCGGGTTCTAGAAAGATATGGATCTGAGAACTGGATG  
GATGATGACAAGGTTGATGTGATTTTCAGCTTCTAGSAGATATG-----AGAACTGGATA

\* 1520 \* 1540 \* 1560  
TCCTCAGCCAGGCATGAACCTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAACATA  
TCCTCAGGTAGGCATGGACCTACTTGCACGGATTTGCTTTCTGGCTTTGGGACAACATA

\* 1580 \* 1600 \* 1620  
GATCCATCCCATGGTCAGCGGATACCTTTTTTATGACCATT---CATCATCACCTTCTATG  
GAACCACTCAGGGTCATCAGATACCTTTTTTATGACCCTTTATCATCACCTTCTGTG

\* 1640 \* 1660 \* 1680  
CCTGCAAGAGGAATCTTGAGTGAATTCAGAGGCAAGTTGGATTATCTTGCTAACCACTGG  
CCTGCAAGGAAATCTTGAGCGACCAAGGATGGCAAGTTGAATATCTTGCTAACCACTGG

\* 1700 \* 1720 \* 1740  
CAGATGATACACTCTGGTCTCTCCCTGAAGTTACATGAATCTCCTAAGGTACCTGCAGCA  
---ATGATSCACTCAGGCCTTCTCCCTGAAGTTACATGAATCTCCTAAGGTACCTGCAGCA

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\* 1760 \* 1780 \* 1800  
ACTGATGCCGTCTCTCCAAGGGCCGATGCAATGTTAAATACAGCGAATATCCTGTTCTTAAT  
TCGATGCCGTCTTCCAAGGGATAGGCAATCCCAATACGGCGAATATGCTTTGCCCTCGT

\* 1820 \* 1840 \* 1860  
GGTCTATCGACTGAGAATGCTGCTGGTAACTGGCCAATACGTCCACGTGCTTTGAATTAT  
GCAGTGAACGACTGAGAATGCTGCTGGCAACTGGCCAATACGTCCACGTGCTCTAAATTAT

\* 1880 \* 1900 \* 1920  
TATGAGGAAGTGGTCAATGCTCAAGCGCAAGGCTCAGGCTAGGGAGCAAGTAACAAAACAA  
TTTGAAGAAGCGGT-----TCAT-----GCTCAGGCTAGAGAGCATGTGACAAAACGT

\* 1940 \* 1960 \* 1980  
CCCTTCA--CGATACAAGAGGAGACAGCAAAGTCAAGAGAGGGGAAGTGCAGGCTCTTTG  
CC-TCCGGTCC-TACAAGAGGAGGCAGCAAAGCCAAGAGACGGGAAGTGCAGGCTTTTG

\* 2000 \* 2020 \* 2040  
GCATTCTCTGACCAACAACATGAATGGGACAGACTCAACCATGTCTCAGAGAAACAACCT  
GCATTCTCTGCTGAACAACGTGAATGGGACAGATACAACTTTGTCTCAGAGAAACAATT

\* 2060 \* 2080 \* 2100  
TGAATGATGCTGCGGGGCTTACACAGATAGCATCACCAAGGTTTCAGGACCTTTTCAGATC  
TGAATGACCTGCGGGGCTTACGCAGATGSCATCACCAAGGTTTCAGGATCTTTCTGACC

\* 2120 \* 2140 \* 2160  
AGTCAAAAGGGTCAAAATCAACAAACGATCATCGTGAACAGGGGAAGACCATTCAGACTA  
AGTCAAAAGGGTCAAAATCGACAAATGATCATCGTGAGCAAGGACGACCATTCCTGCTTA

\* 2180 \* 2200 \* 2220  
ATAATCCTCATCCGAAGGATGCTCAAACGAAAACCAACTCAAGTAGGAGTTGCACAAAGG  
GTAAACCCCATCCGAAGAGCGTTCAAACGAAAACCAAACTCATGTAGGAGCTGCACGAAGG

\* 2240 \* 2260 \* 2280  
ITTCACAAGCAGGGGAATTGCACTTGGCCGTTTCAGTGGATCTTTCAAAGTTCCAAAACCTATG  
ITTCAGAAGCAGGGGATTGCACTTGGCCGTTTCAGTGGATCTCTCAAAGTTCCAGAACTATG

\* 2300 \* 2320 \* 2340  
AGGAGTTTASTCGCTGAGCTGGACAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTA  
AGGAGTTGCTTACTGAATTGGATAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTA

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\* 2360 \* 2380 \* 2400  
AGAAAGATTGGT TGATAGTTTACACAGATGAA GAGAATGATATGATGCTTGTGGT GACG  
AGAAAGATTGGT TGATAGTTTACACAGATGAT GAGAATGATATGATGCTTGTGGT GACG

\* 2420 \* 2440 \* 2460  
ATCCTTGGCAGGAGTTTTGTTGCATGGTTCC AAAATCTTCATATACACGAAAGAGGAAG  
ATCCTTGGCAGGAGTTTTGTTGCATGGTTCC AAAATCTTCATATACACGAAAGAGGAGG

\* 2480 \* 2500 \* 2520  
TGAGGAAGATGAACCCGGGGA ACTTTAAGCTCTTAGGAG CGAGGAAGAAG CAGTTGTTGGGG  
TGAGGAAGATGAACCCGGGGA ACTTTAAGCTCTTAGGAG CGAGGAAGAAG CAGTTGTTGGGG

\* 2540 \* 2560 \* 2580  
AAGGATCAGATGCAAAGGACGCCAAGTCTGCATCAAATCCTTCATTGTCCAGCGCTGGGA  
AAGGATCAGATGCAAAGGACGCCAAGTCTGCATCAAATCCTTCATTGTCCAGCGCGGGA

ACTCTTAA  
ACTCTTAA



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# Figure 9

## Alignment of MNT, BnARF2, OsARF2 proteins

```

      *           20           *           40           *
MNTwt : MASSEVSMKGNRC-EDNFSSSGFSDEPKETRNVSVAGEGQKSNSTRSAAAEALDIP
BnARF2: MASSEVSMKGNRCRENFSSAGYSDE-----TVAGEAQKTSNRSVAAERVVDP
OsARF2: -----GDP

      60           *           80           *           100          *
MNTwt : EAALYRELWHACAGPLVTVPRQDDRVFYFPOGHIEQVEASTNQAAEQOMPLYDLIP
BnARF2: EAALYRELWHACAGPLVTVPRQDDRVFYFPOGHIEQVEASTNQAAEQOMPLYDLIP
OsARF2: ---LYDELWHACAGPLVTVPRVGDLVFYFPOGHIEQVEASMNQVADSOMRLYDLIP

      120          *           140          *           160
MNTwt : SKILCRVINVDLKAEADTDEVYAQITLLPEANODENATEKEAPLPPP--PRFOVH
BnARF2: SKILCRVINVDLKAEADTDEVYAQITLLPEPVODENSIEKEAPPPP--PRFOVH
OsARF2: SKILCRVINVELKAEQDTDEVYAQVLMMPPEEONEMAVEKITPTISGRVQARPPVR

      *           180          *           200          *           220
MNTwt : SFCKTLTASDTSTHGGFSVLRRHADECLPPLDMSROPPTQELVAKDLHANEWRFR
BnARF2: SFCKTLTASDTSTHGGFSVLRRHADECLPPLDMSROPPTQELVAKDLHASEWRFR
OsARF2: SFCKTLTASDTSTHGGFSVLRRHADECLPPLDMTQSEPTQELVAKDLHSMDWRFR

      *           240          *           260          *
MNTwt : HIFRGQPRRHLLQSGWSVFVSSKRLVAGDAFIFLRGENGELRVGVRRAMROQENV
BnARF2: HIFRGQPRRHLLQSGWSVFVSSKRLVAGDAFIFLRGENGELRVGVRRAMROQENV
OsARF2: HIFRGQPRRHLLQSGWSVFVSSKRLVAGDAFIFLRGENGELRVGVRRAMROLNSV

      280          *           300          *           320          *
MNTwt : PSSVISSHSMLGLVLATAWHAIISTGIMFTVYYKPRTSPSEFIIVPFDOYMESVKNN
BnARF2: PSSVISSHSMLGLVLATAWHAIISTGIMFTVYYKPRTSPSEFIIVPFDOYTESVKIN
OsARF2: PSSVISSQSMHLGLVLATAWHAINIKSMFTVYYKPRTSPSEFIIVPFDOYMESVKNN

      340          *           360          *           380
MNTwt : YSIGMRFKMRFEGEEAPEQRFTGTITVGIEESDPTRWKSKWRSCLKVRWDETSSIP
BnARF2: YSIGMRFKMRFEGEEAPEQRFTGTITVGIEDSDPTRWAKSKWRSCLKVRWDETTSIP
OsARF2: YSVGMRFKMRFEGEEAPEQRFTGTITLGSENLDPV-WPESSWRSLKVRWDEPSTIP

      *           400          *           420          *           440
MNTwt : RPDRVSPWKTEPALAPPALSPVPMRPFKRPRSNLAPSSPDSSMITREGTITKANMD
BnARF2: RPDRVSPWKTEPALSPPALSPVPMRPFKRPRSNLASSTPDSSMRITREGSSKANMD
OsARF2: RPDRVSPWKTEPASPP-VNPLPLSRVKRPRPNAPPASPESPITIKKAAAKVDTD

```

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```

      *           460           *           480           *
MNTwt : PLPA--SGLSRVLOGQEYSTLRKHTESVECDAPENS-VVWQSSADDDKVDVVSg
BnARF2: PLPA--SGLSRVLOGQEYPTLRKHVESVECDAPENS-VVWQSSADDDKVDVISA
OsARF2: PAQAQRSQNSTVLQGQEQMTLRSNLTESNDSQDVTAKHKKMMWSPSPNAAKAHPLTF

```

```

      500           *           520           *           540           *
MNTwt : SRRYGSENWMSSARHEPTYTDLLSGFGTNIDPSHGQRIFFYDH-SSSPSMPA-KR
BnARF2: SRRY--ENWISSGRHGPTCTDLLSGFGTNIEPPHGHQIRFFYDRLSSPPSVAA-RK
OsARF2: QQRPPMDNWMQLGRRETDFKDVRSQ-SQSEFGDSPGFFMQNFDE--APNRLTSFKN

```

```

      560           *           580           *           600
MNTwt : ILSDSEGGFDYLANQFMTHSGLSIKLHE SPKVPAAATDASLOQRONVKEYSEMPVL
BnARF2: ILSDQDGGFEYLANQFMTHSGLSIKLHE SPKVPAAADASFQIGNPNYGEMALP
OsARF2: QFQDQ-GSARHFSDPYYYV-----SPOPSLTVESSTQMHTDSK--ELHFW

```

```

      *           620           *           640           *           660
MNTwt : NGLSTENAGGNWPTRPRALNYEYEVVNAQAQAQAR-EQ--VLKQFETIQE-ETAK
BnARF2: RAVTTENAAGNWPTRPRALNYEFAVHAC----AR-EH--VTKRRRAVVQE-EAAK
OsARF2: NGOST--VYGNSRDRPQNFRFEQNSSSWLNQSFARPEQPRVIRPHASTAPVELEK

```

```

      *           680           *           700           *
MNTwt : SREGNCRHFGIEL-NNNM--NETDSTMSQENNN--LNDAAAGITQIASPKVQDLSDQ
BnARF2: PRDGNCRHFGIEL-VNNV--NETDTILSQENNN--LNDPAGPIQMASPKVQDLSDQ
OsARF2: TEGSGFKIDGFKVDITNAPNNHLS SPMATHEPMLQTES SLNQLQPVQTDCEPEV

```

```

      720           *           740           *           760           *
MNTwt : SKGSKSTNDHREQGRPFQTNNEHPKDAQTKTN--SSRSCTKVHKQGTALGRSVDL
BnARF2: SKGSKSTNDHREQGRPFVSKHHPKDVQTKTN--SCRSC TKVHKQGTALGRSVDL
OsARF2: SVSTAGTATENEKSG--QQAQSSKDVQSKLOVASTRSC TKVHKQGTALGRSVDL

```

```

      780           *           800           *           820
MNTwt : SKFONYEELVAELDRLEFNGELMAPKKDWLIVYTDEENDMMLVGDDPWQEFCCM
BnARF2: SKFONYEELVTELDRLFEFNGELMAPKKDWLIVYTDEENDMMLVGDDPWQEFCCM
OsARF2: SKFSNYDELKAEIDKMFEDGELVSSNKWQIVYTDEEGDMMLVGDDPWQEFCSI

```

```

      *           840           *           860           *
MNTwt : VRKIFITYTKEEVKMNPGTILS CRSEEEAVV GEGSDAKDAKSASNP SLSSAGNS
BnARF2: VRKIFITYTKEEVKMNPGTILC CRNEEEPVV GEGSDAKDAKSASNP SLSSAGNS
OsARF2: VRKITITYTKEEVQKMN SKSNAPRKD-----DSSENEKGHLPMMPNKSDN-

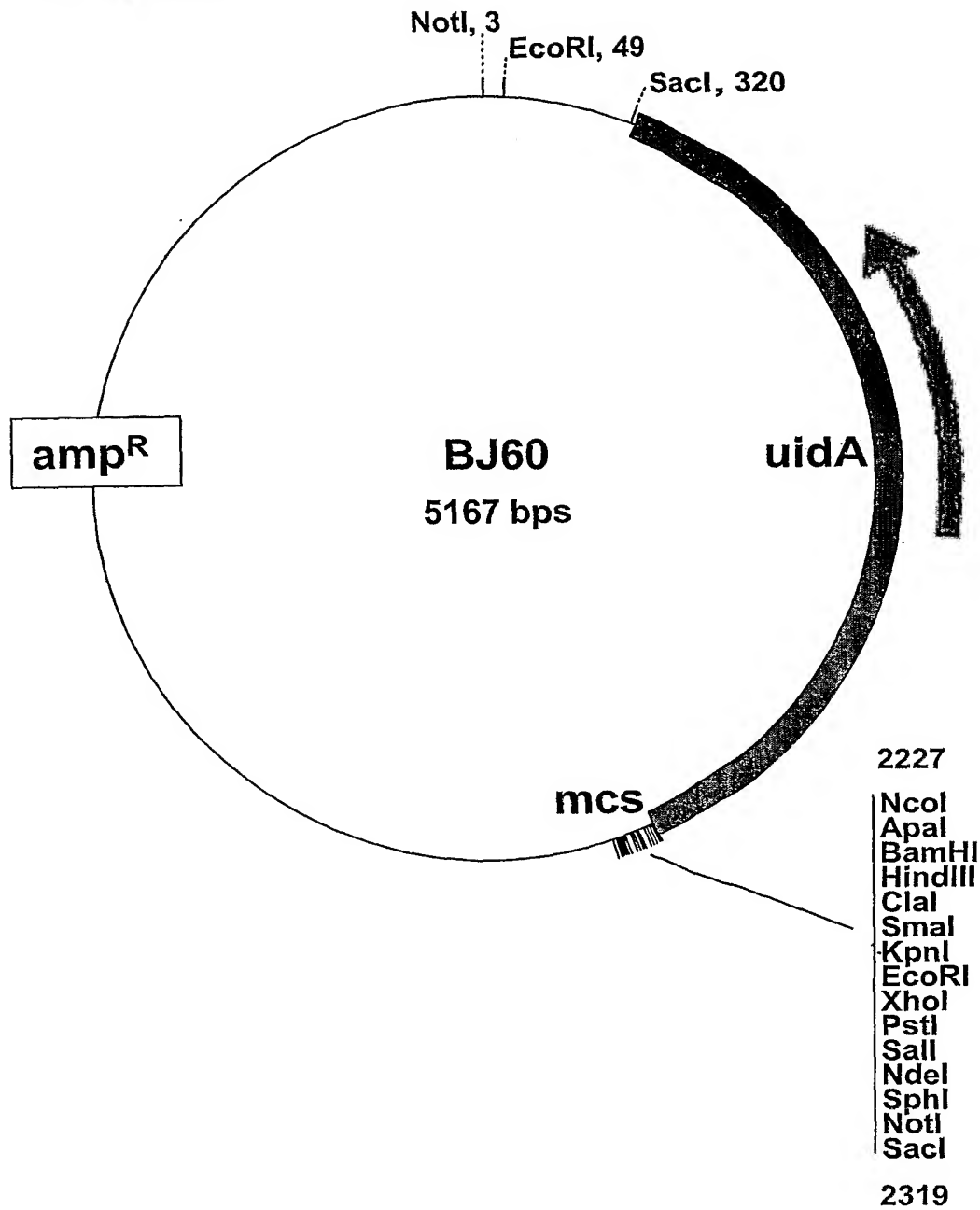
```

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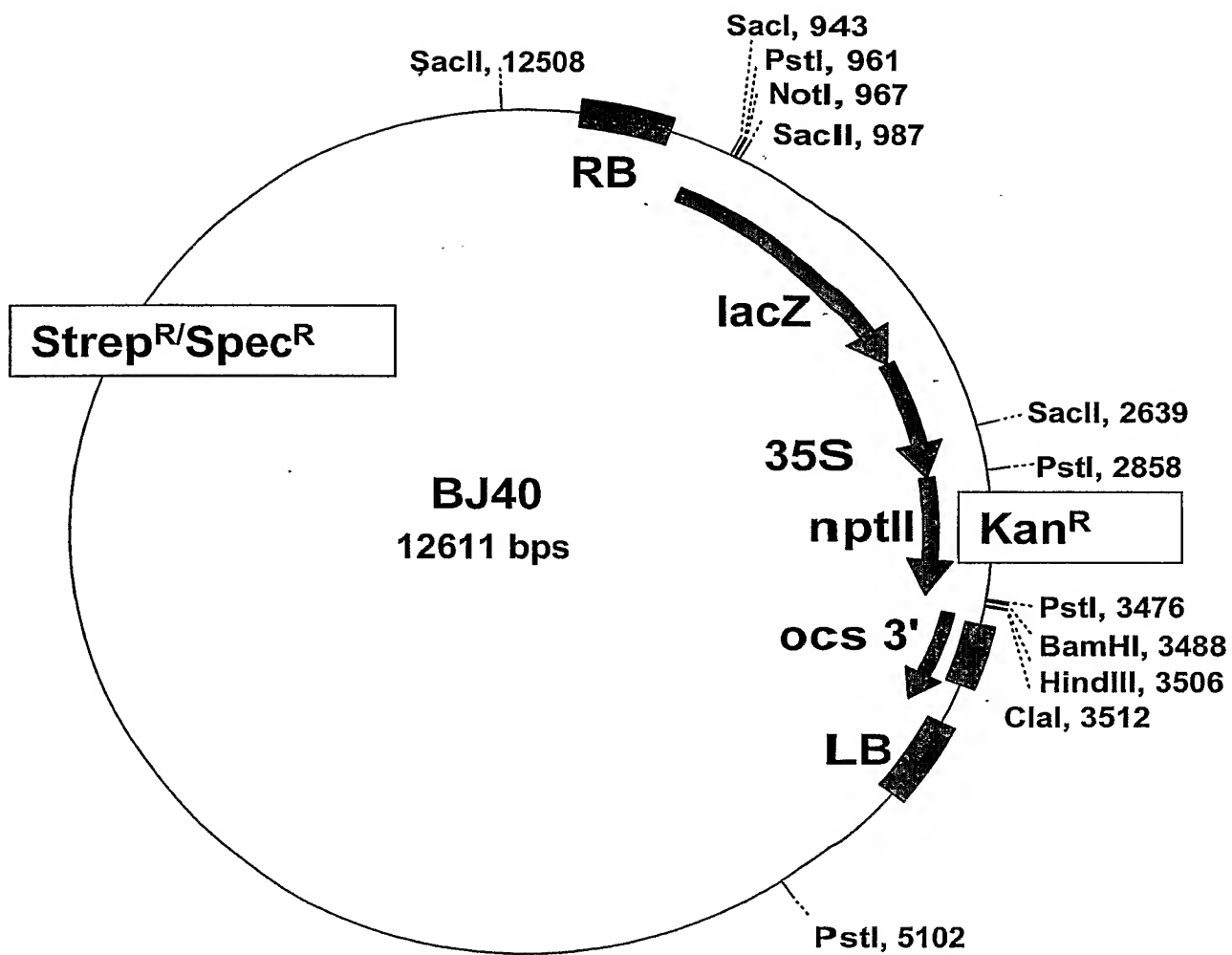
# Figure 10

## Vectors used for cloning

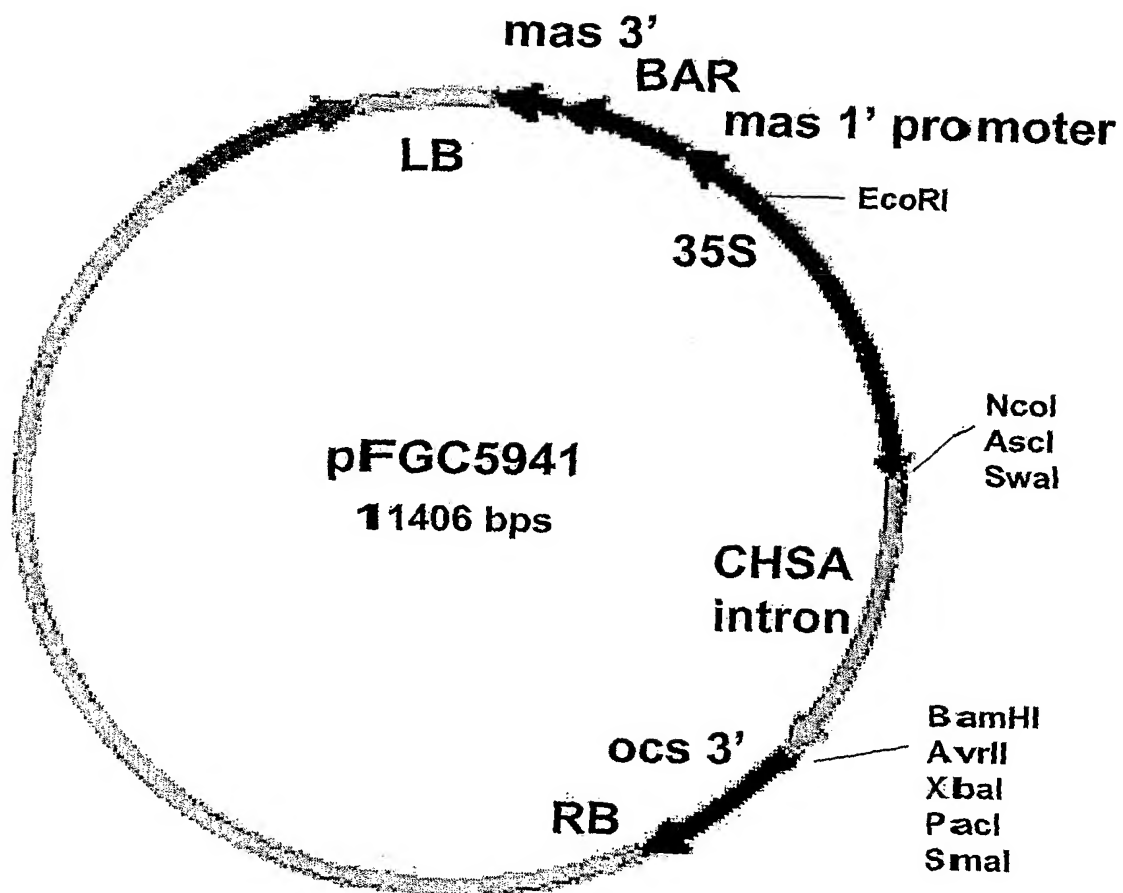
### 10A BJ60



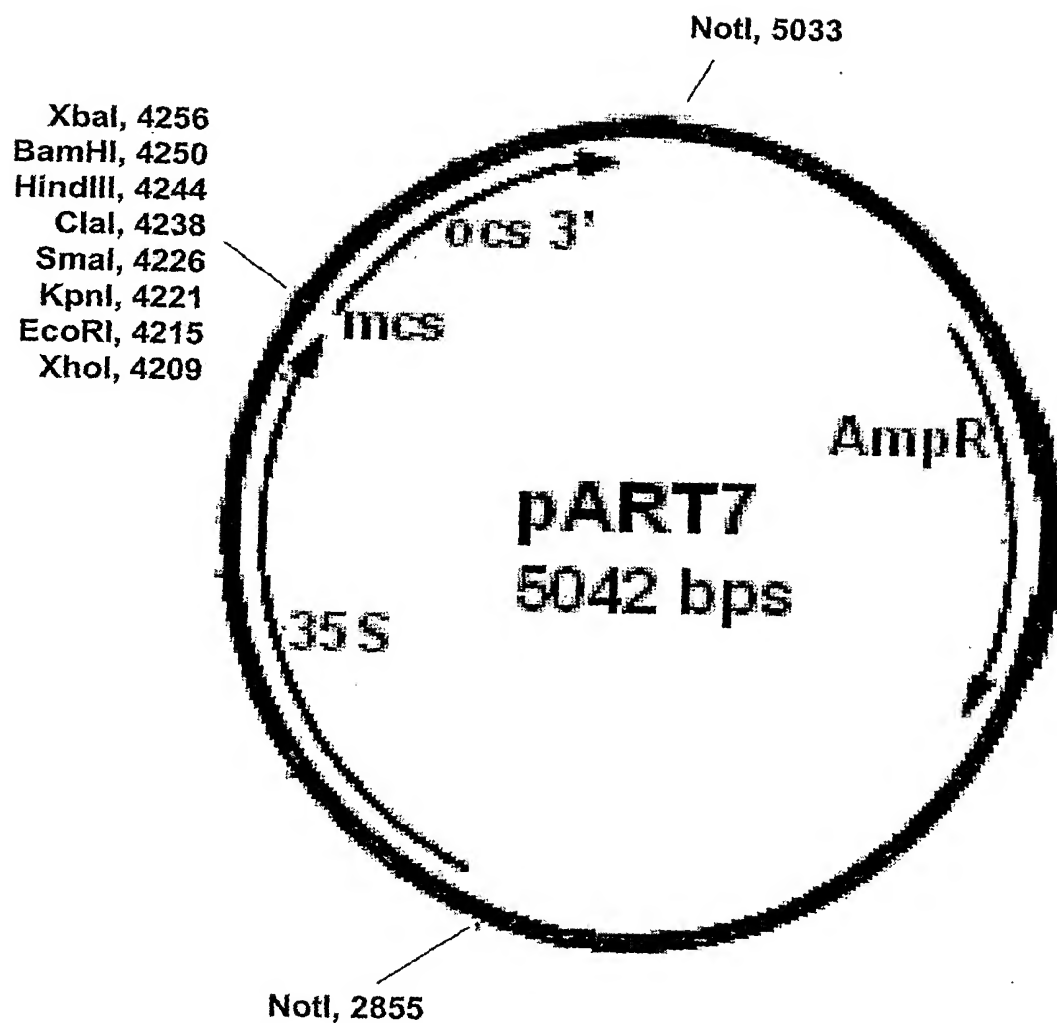
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**10B BJ40**

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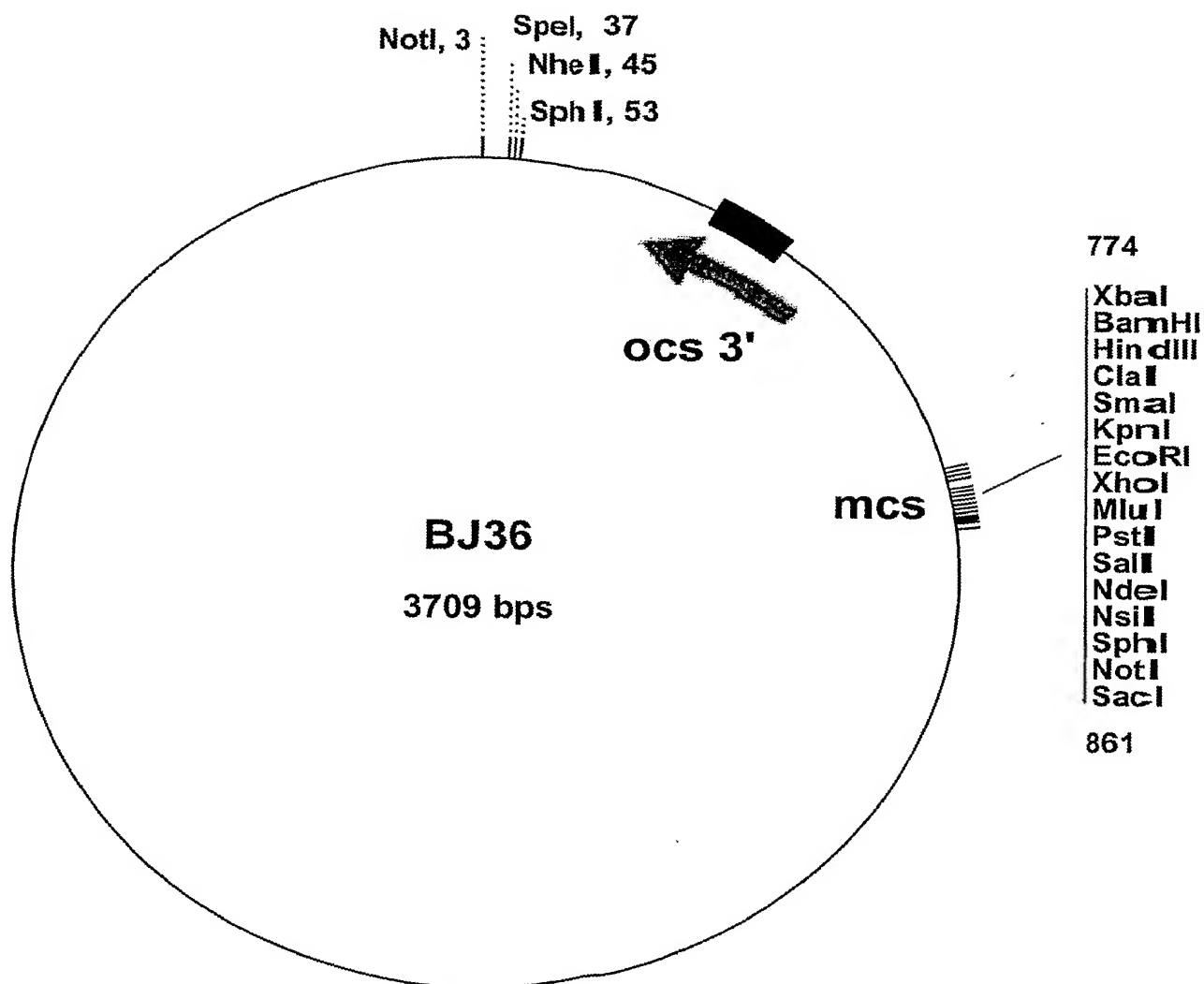
**10C pFGC5941**

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**10D pART7**

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0E BJ36

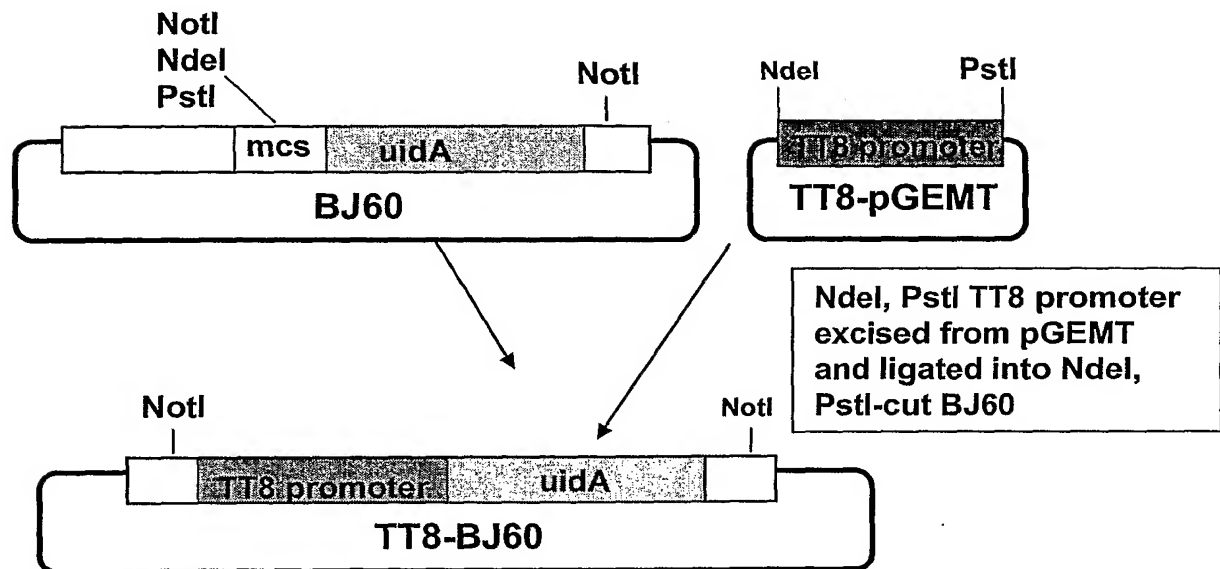




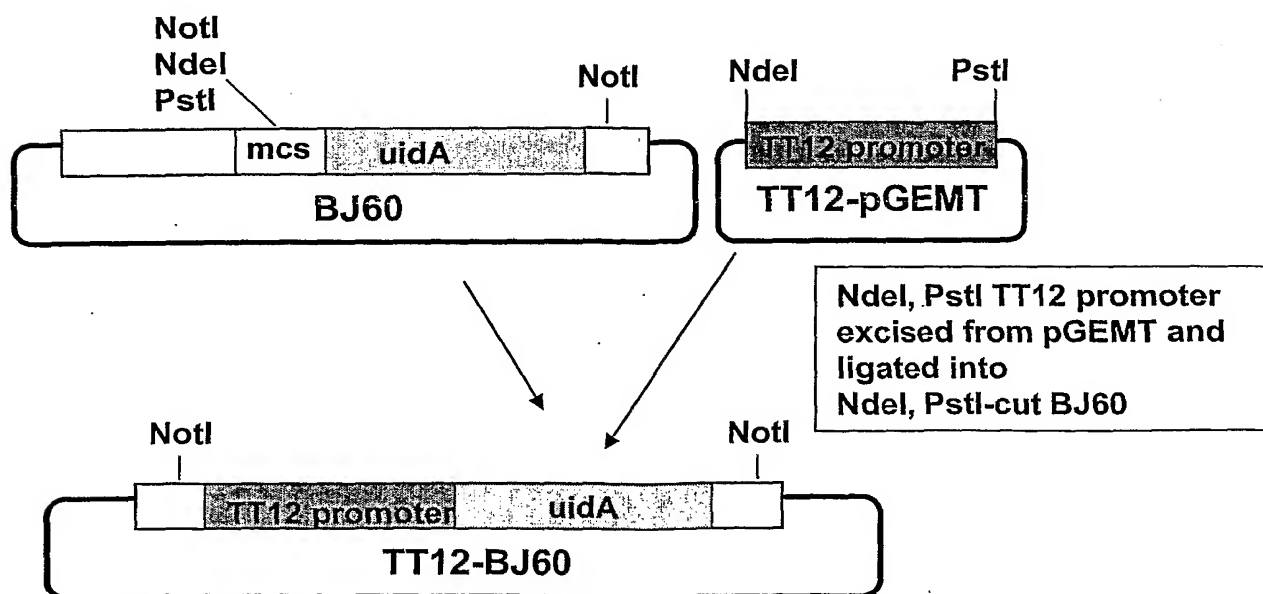
## Figure 11

### Cloning strategy, Example 3

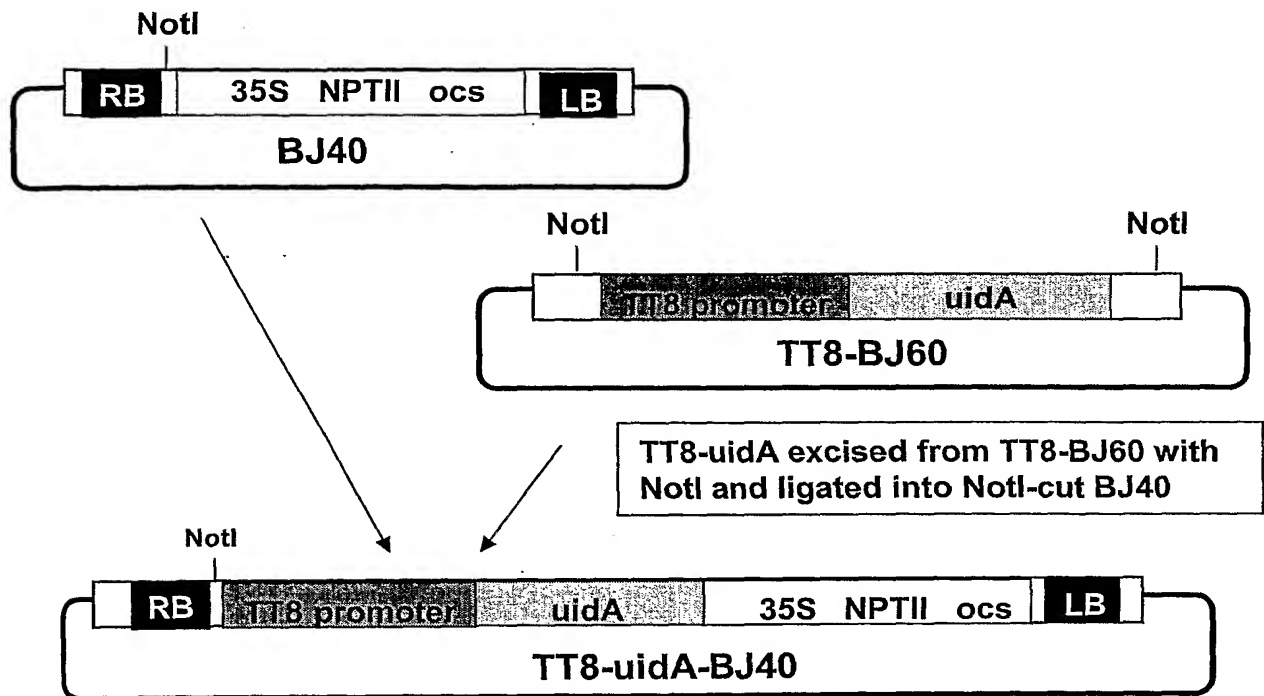
#### Example 3a(i)



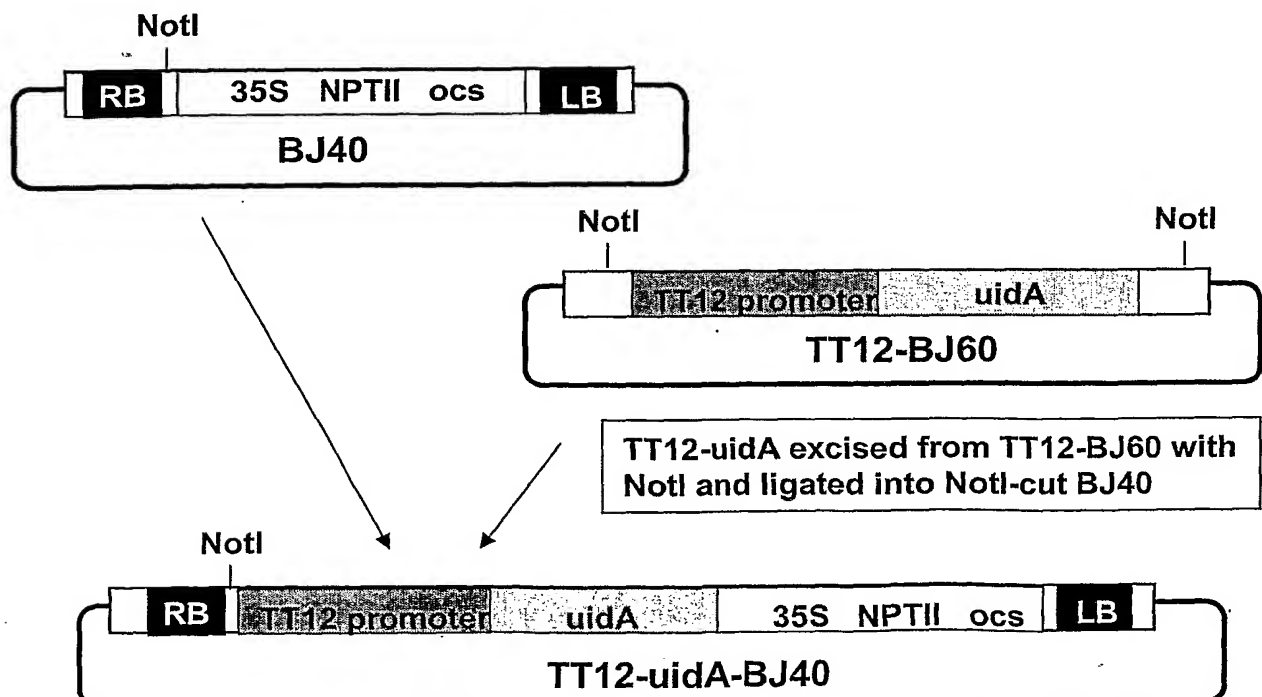
#### Example 3a(ii)



### Example 3b(i)



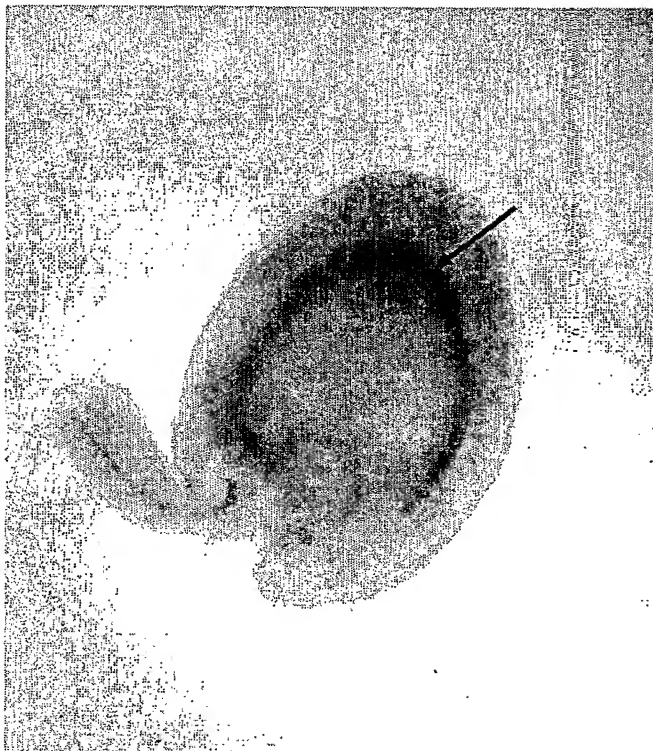
### Example 3b(ii)



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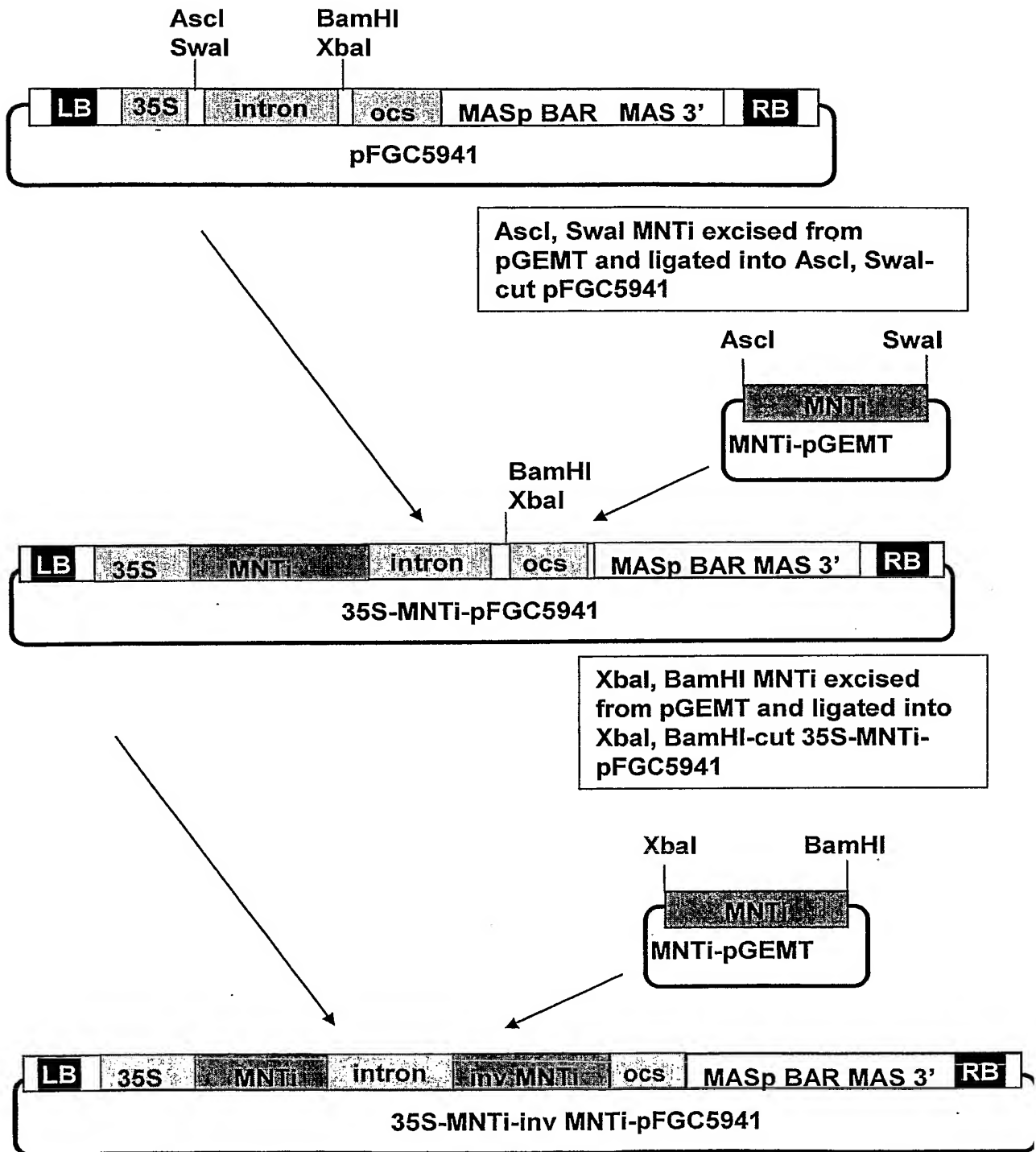
## Figure12

TT12::uidA



## Figure 13A

### Cloning strategy, Example 4

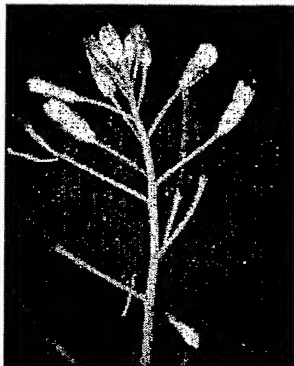


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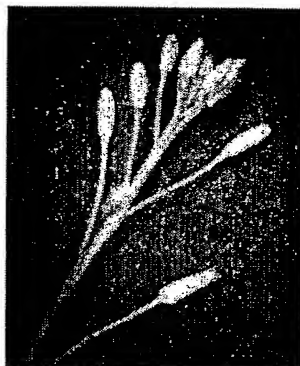
## Figure 13B

Plants transformed with the *35S::MNT* RNAi vector  
Example 4

Primary inflorescence



wild-type Col-3



*35S::MNT* RNAi  
line 3

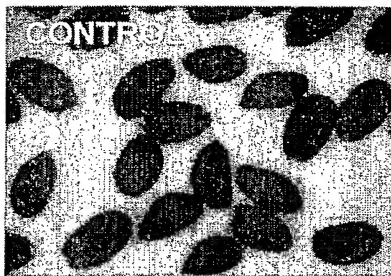
Primary inflorescence stem



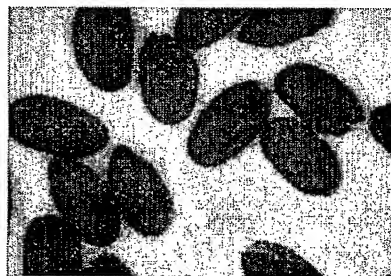
wild-type Col-3



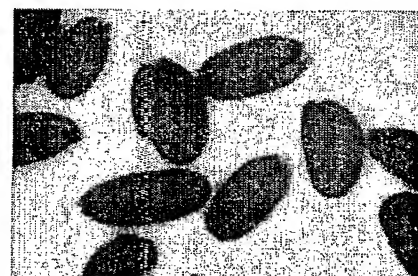
*35S::MNT* RNAi  
line 3



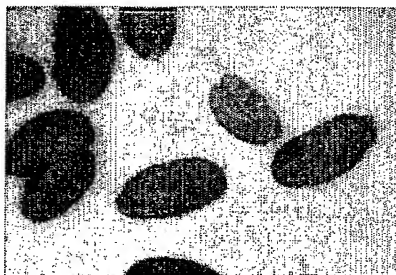
wild-type Col-3  
mean wt 13.8  $\mu$ g



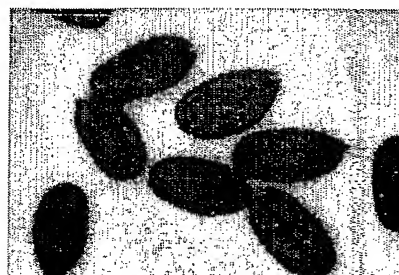
*35S::MNT* RNAi line 1  
mean wt 34.0  $\mu$ g



*35S::MNT* RNAi line 2  
mean wt 35.6  $\mu$ g



*35S::MNT* RNAi line 3  
mean wt 34.8  $\mu$ g

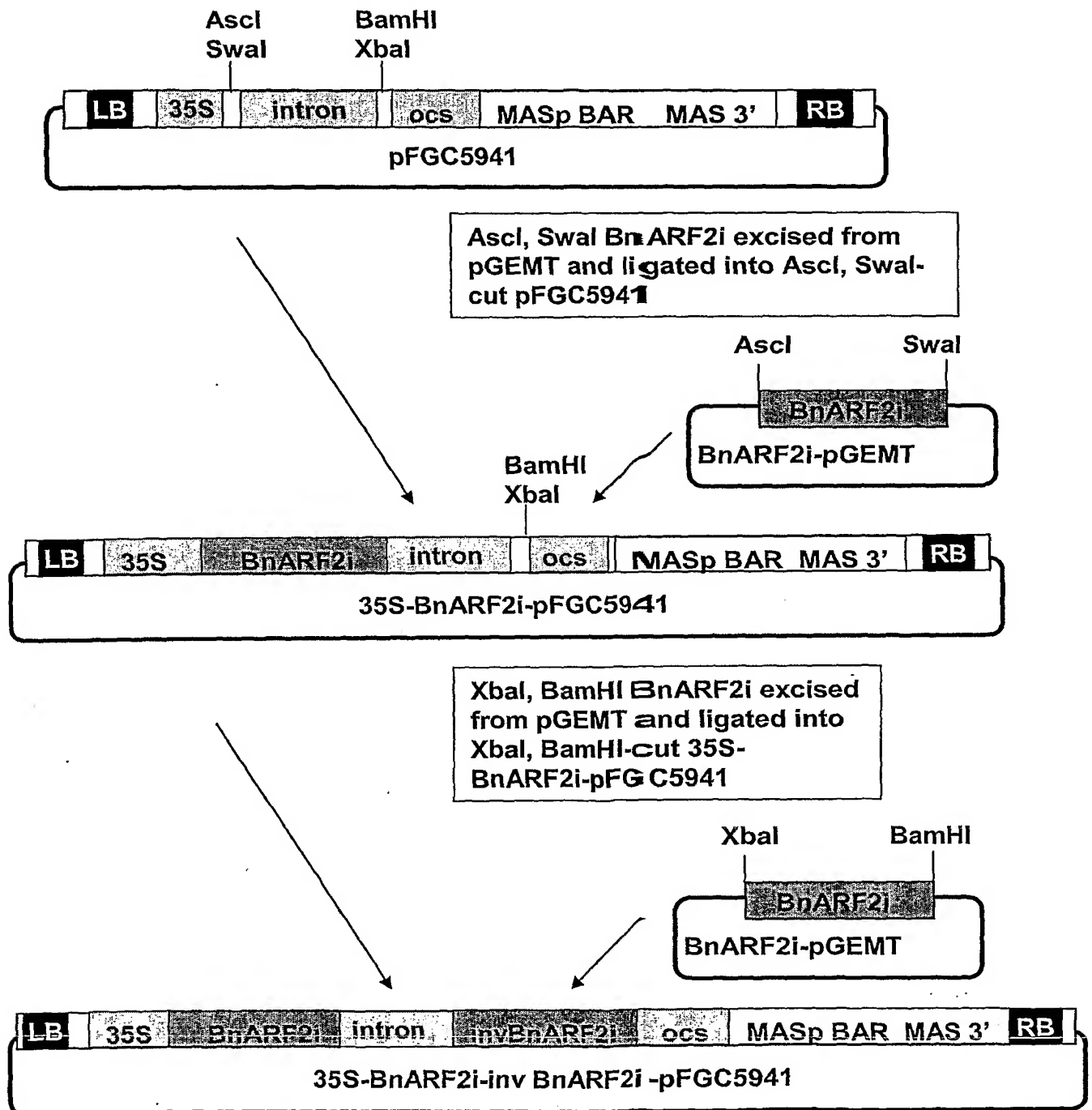


*35S::MNT* RNAi line 4  
mean wt 36.7  $\mu$ g

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## Figure 14

### Cloning strategy, Example 5

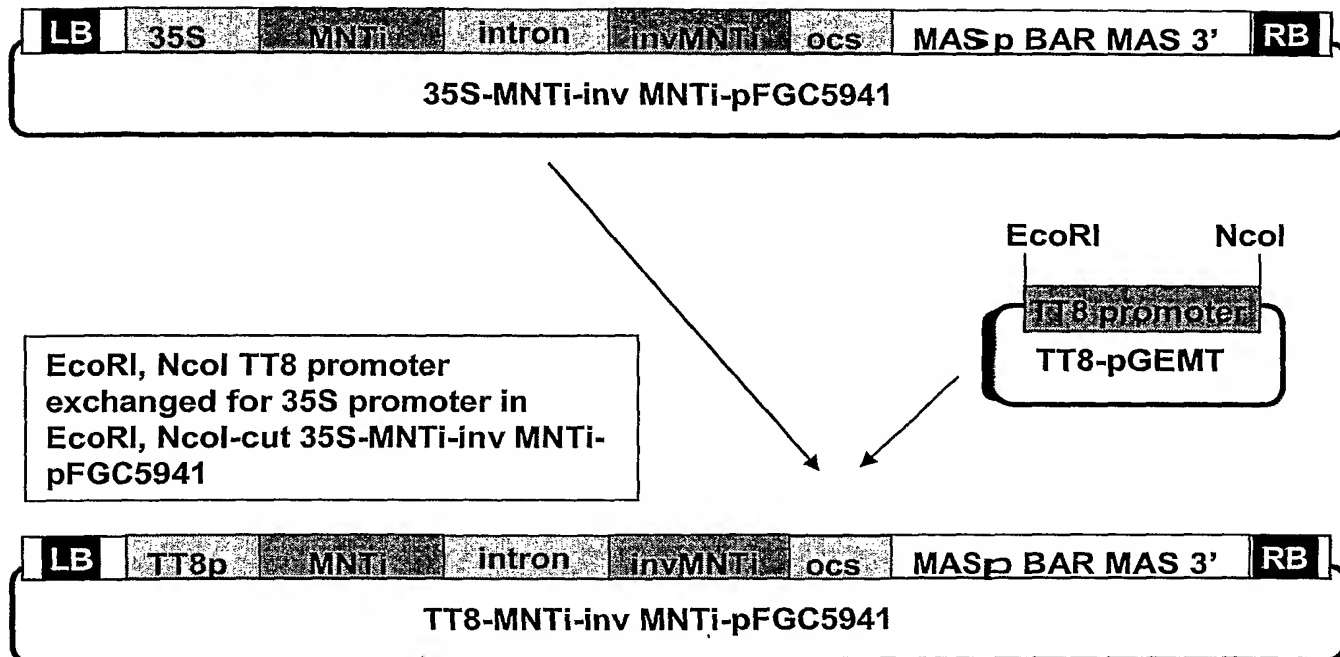


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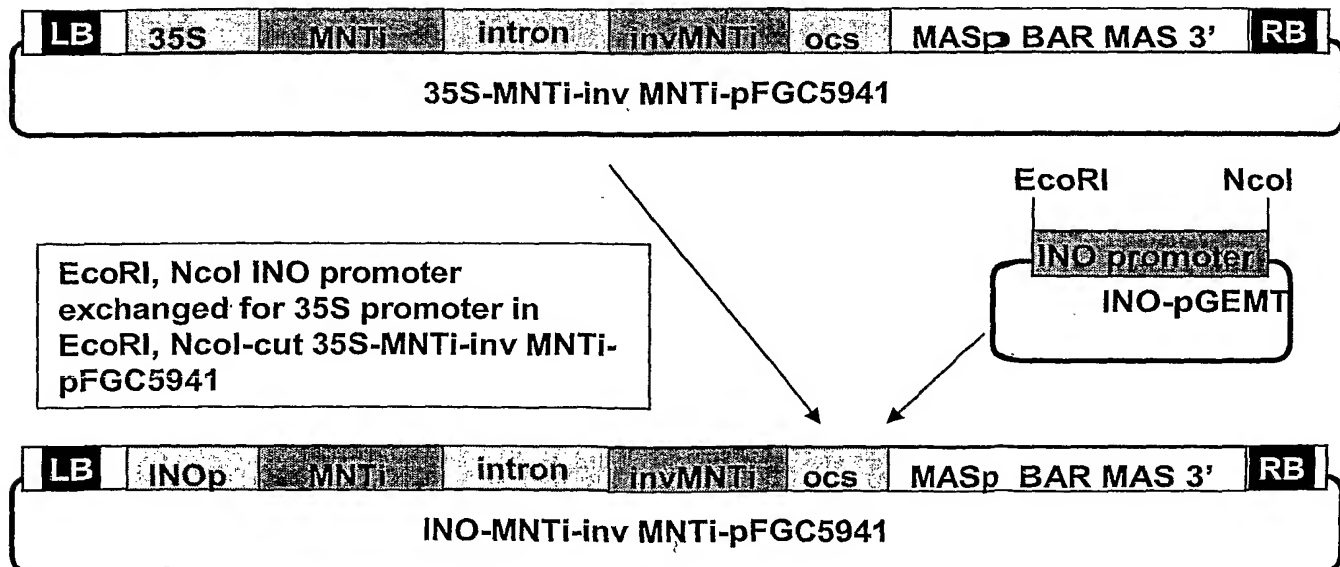
## Figure 15

### Cloning strategy, Example 6

#### Example 6a(i)



#### Example 6a(ii)

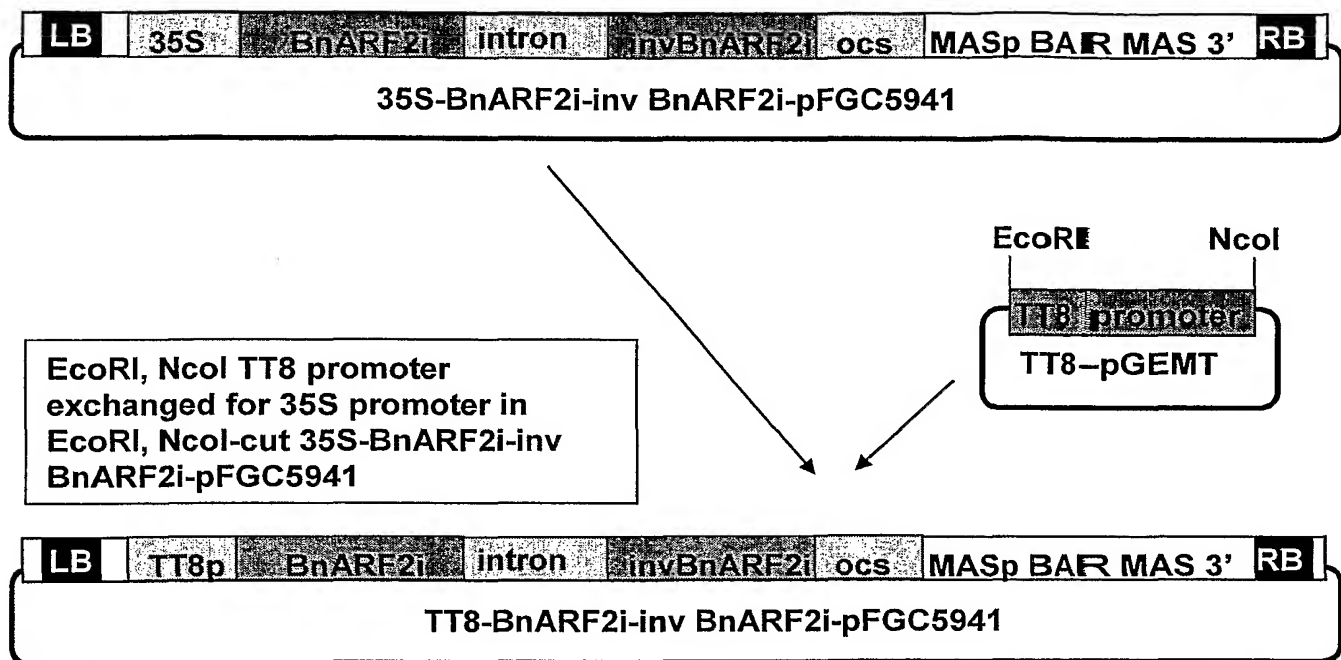




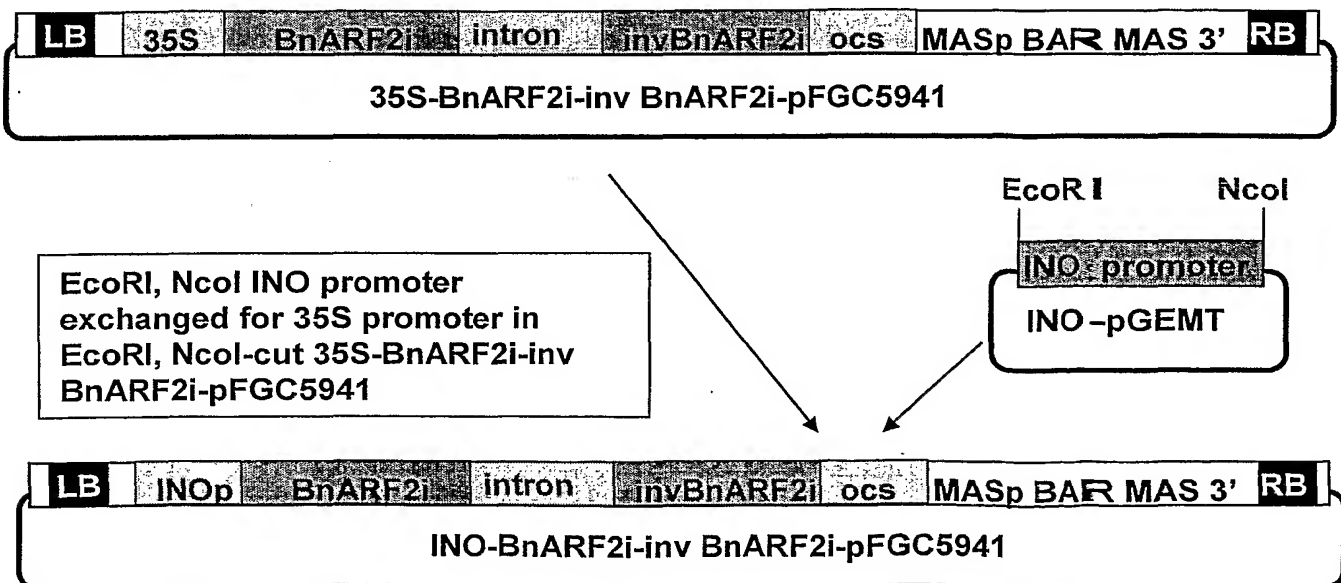
## Figure 16

### Cloning strategy, Example 7

#### Example 7a(i)



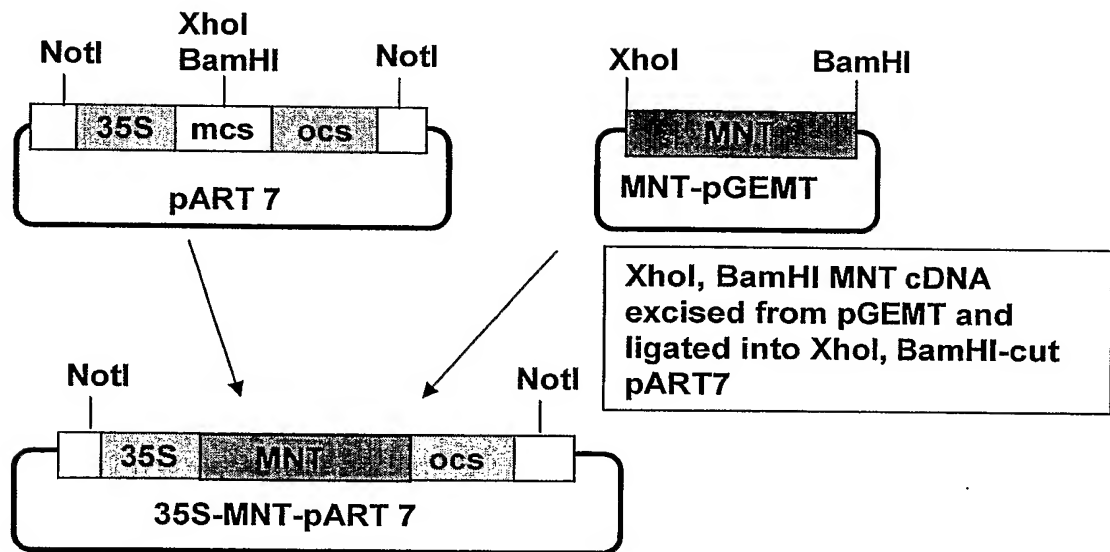
#### Example 7a(ii)



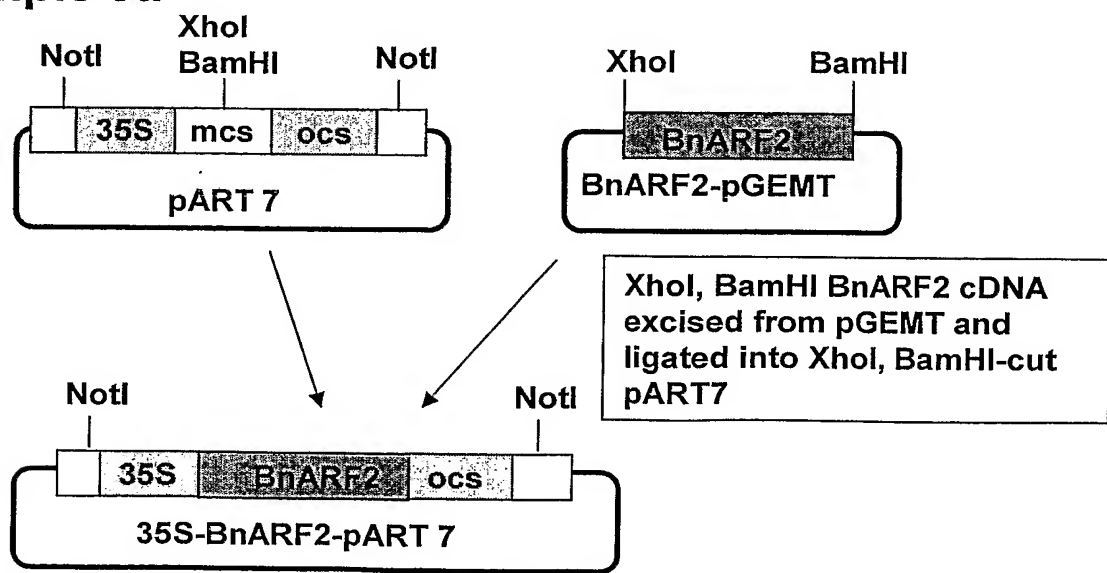
## Figure 17A

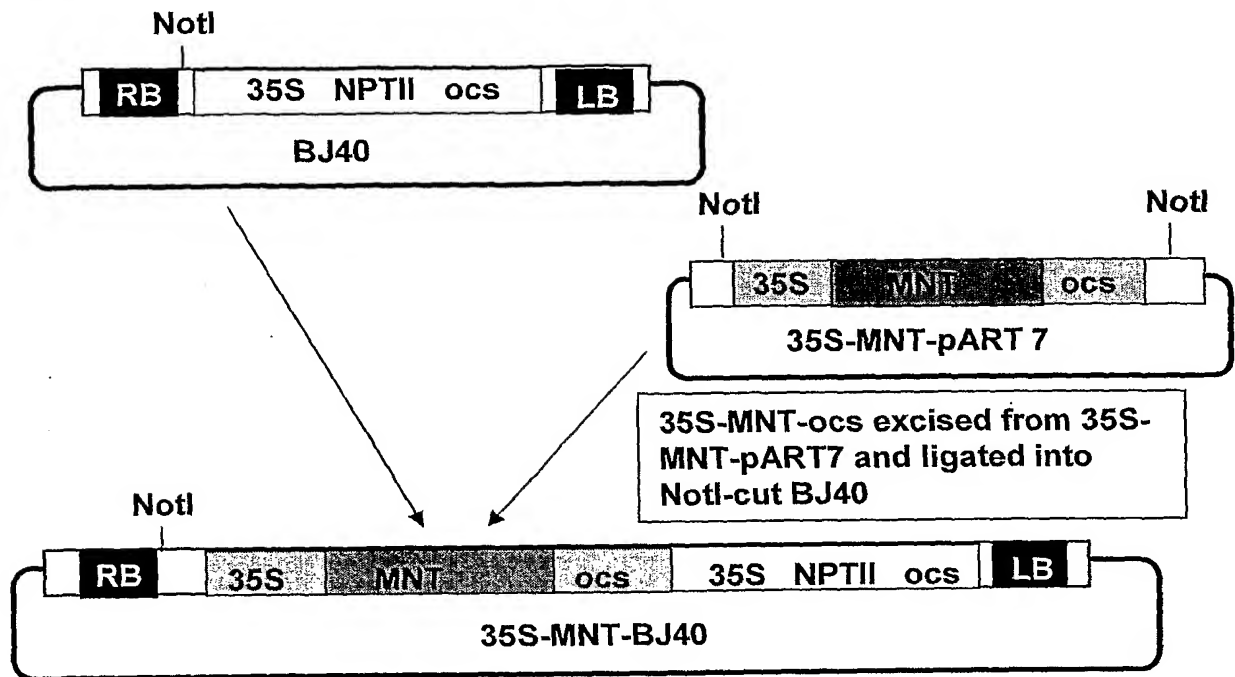
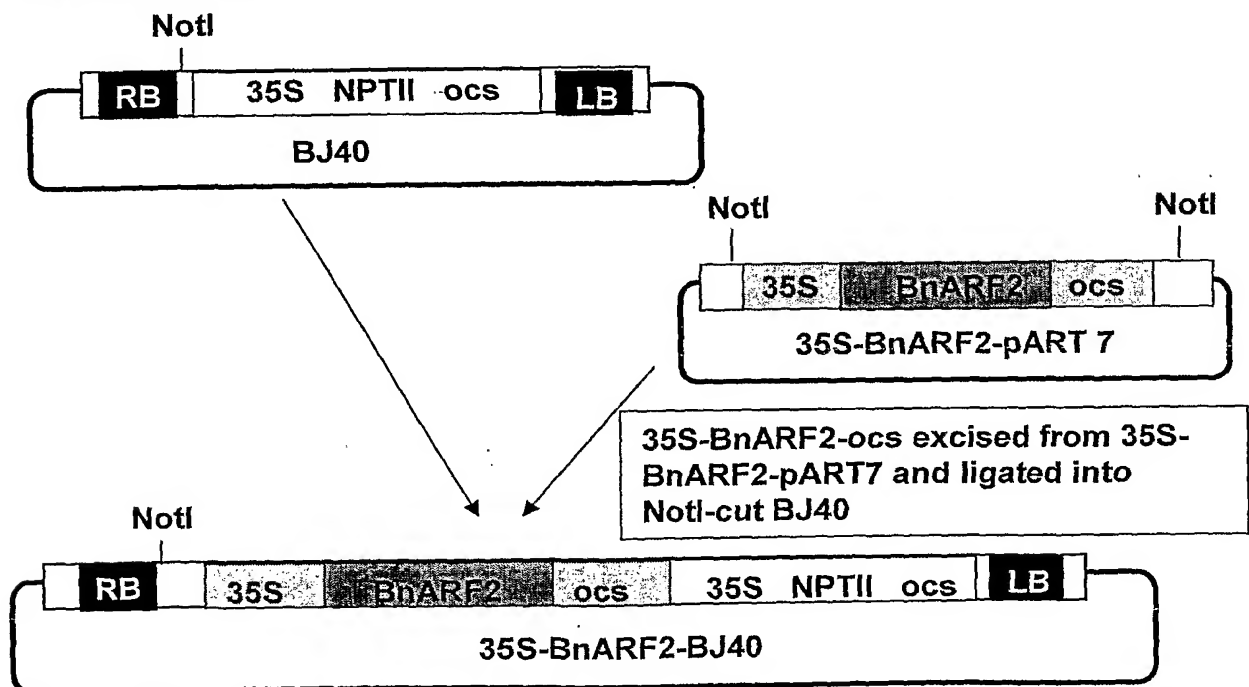
### Cloning strategy, Examples 8, 9

#### Example 8a



#### Example 9a



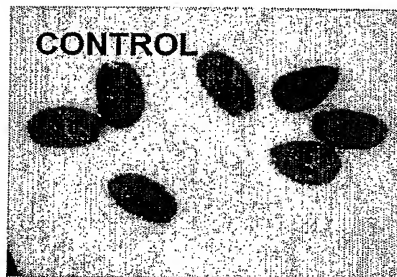
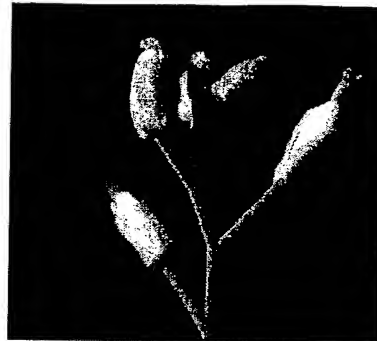
**Example 8b****Example 9b**

## Figure 17B

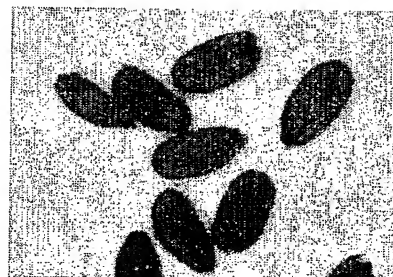
Analysis of wild-type plants transformed with the *35S::MNT* vector

Example 8

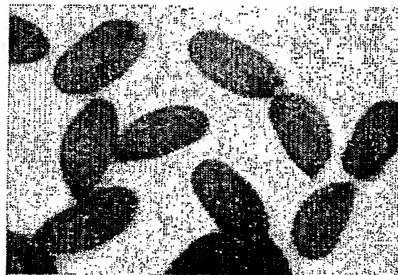
*35S::MNT*



wild-type Col-3  
mean wt 15.0  $\mu$ g



*35S::MNT* line 1  
mean wt 23.1  $\mu$ g

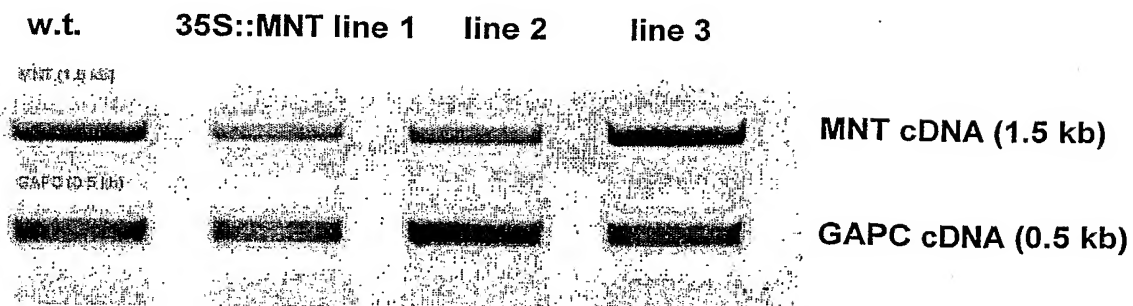


*35S::MNT* line 2  
mean wt 28.7  $\mu$ g



*35S::MNT* line 3  
mean wt 24.6  $\mu$ g

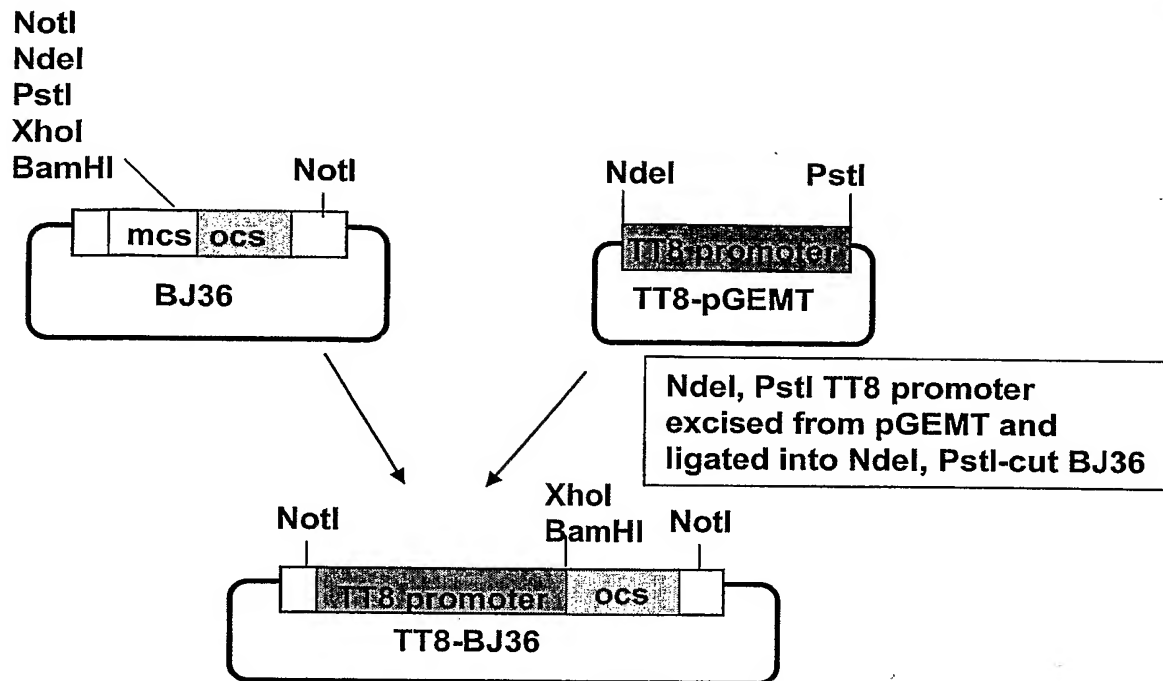
## Semiquantitative RT-PCR



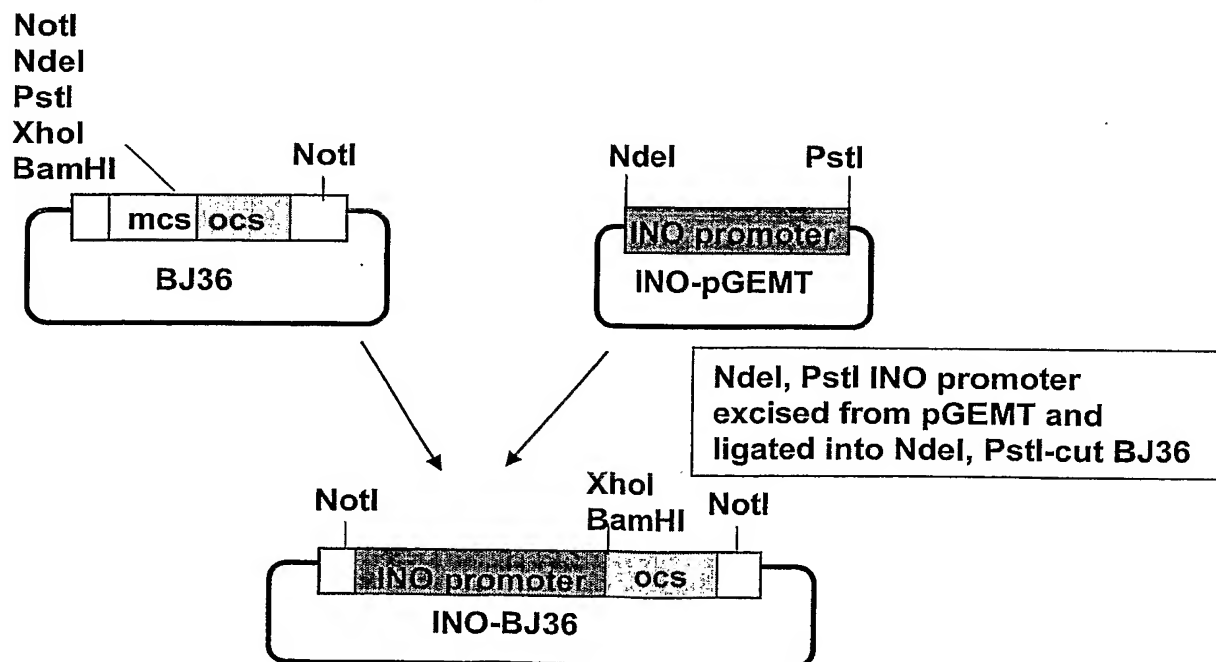
# Figure 18

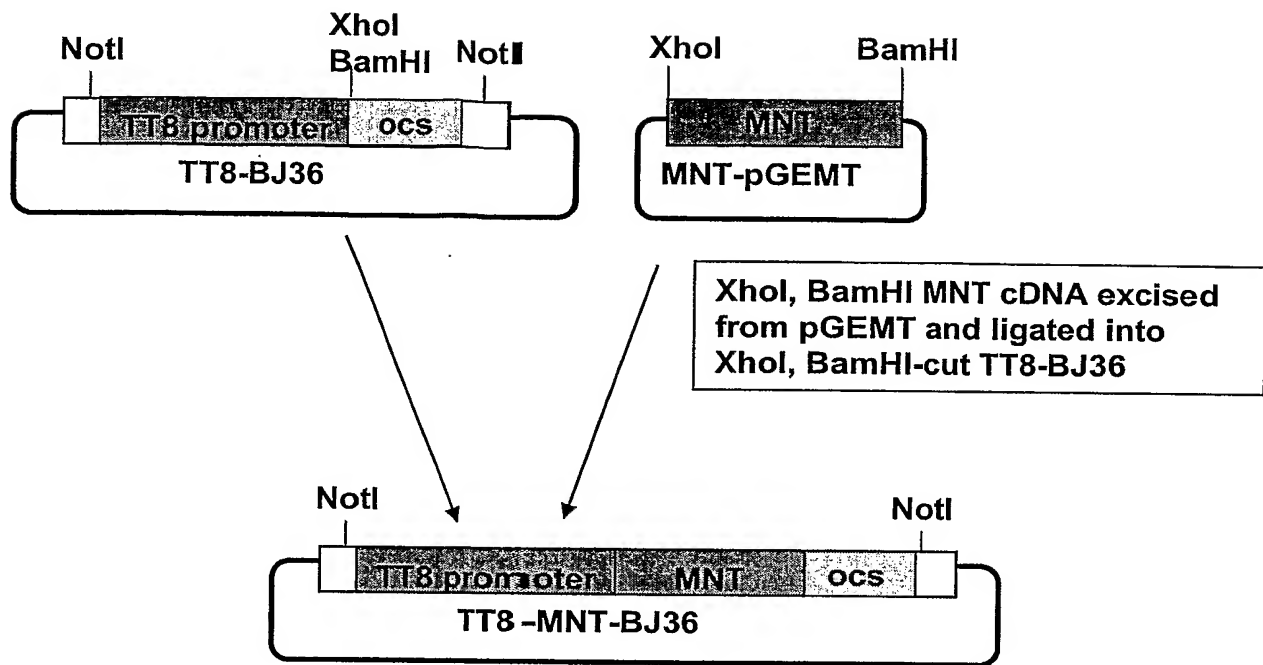
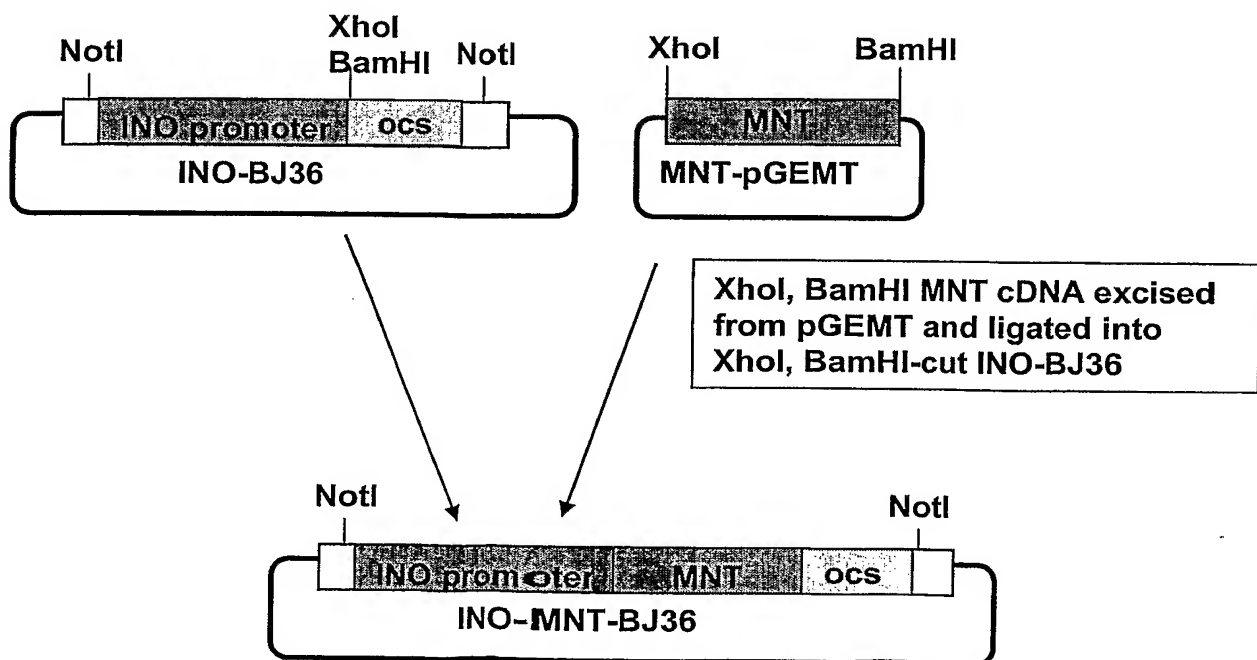
## Cloning strategy, Example 10

### Example 10a(i)

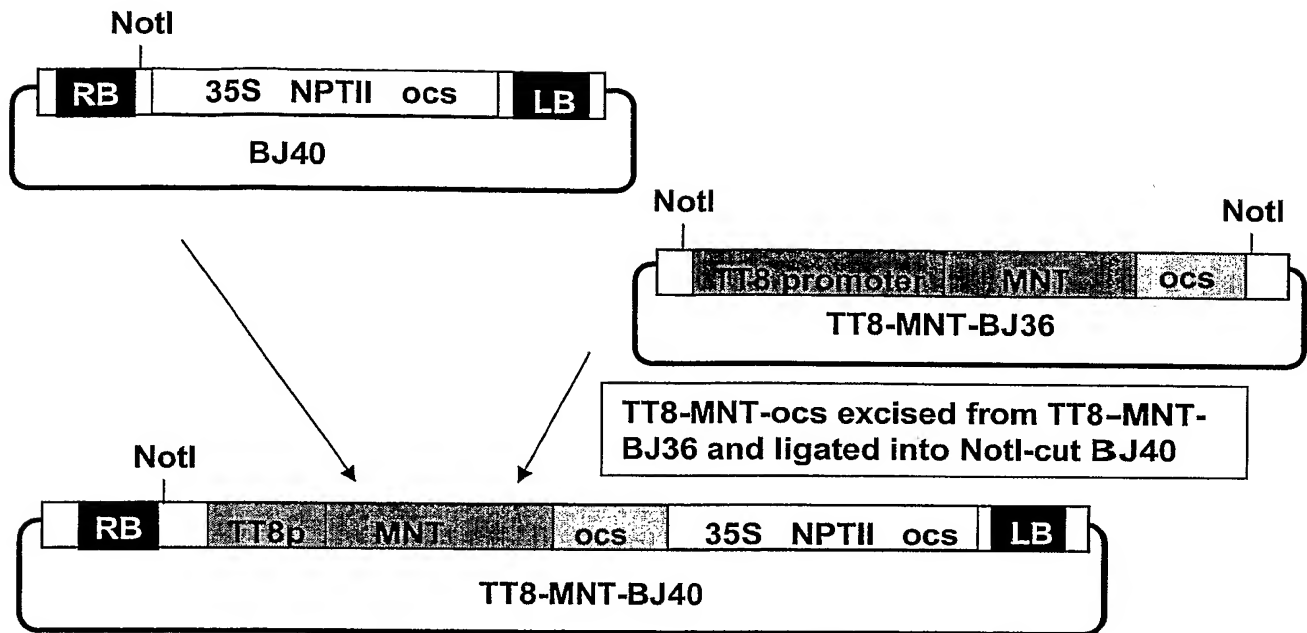
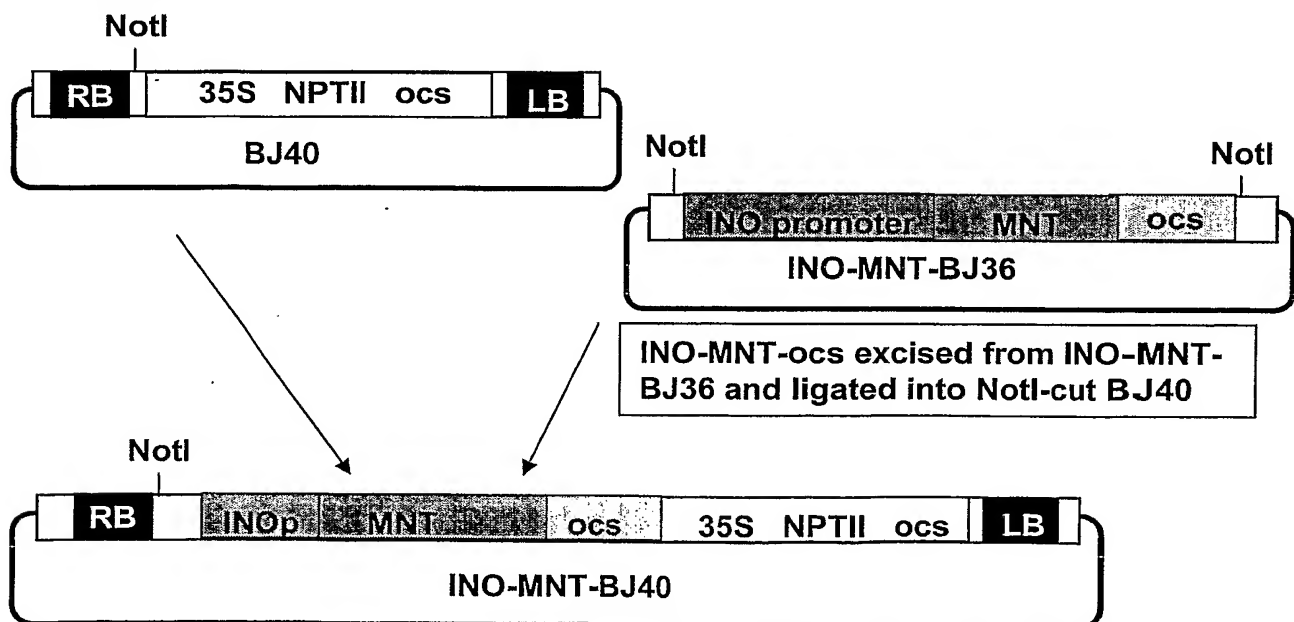


### Example 10a(ii)



**Example 10b(i)****Example 10b(ii)**

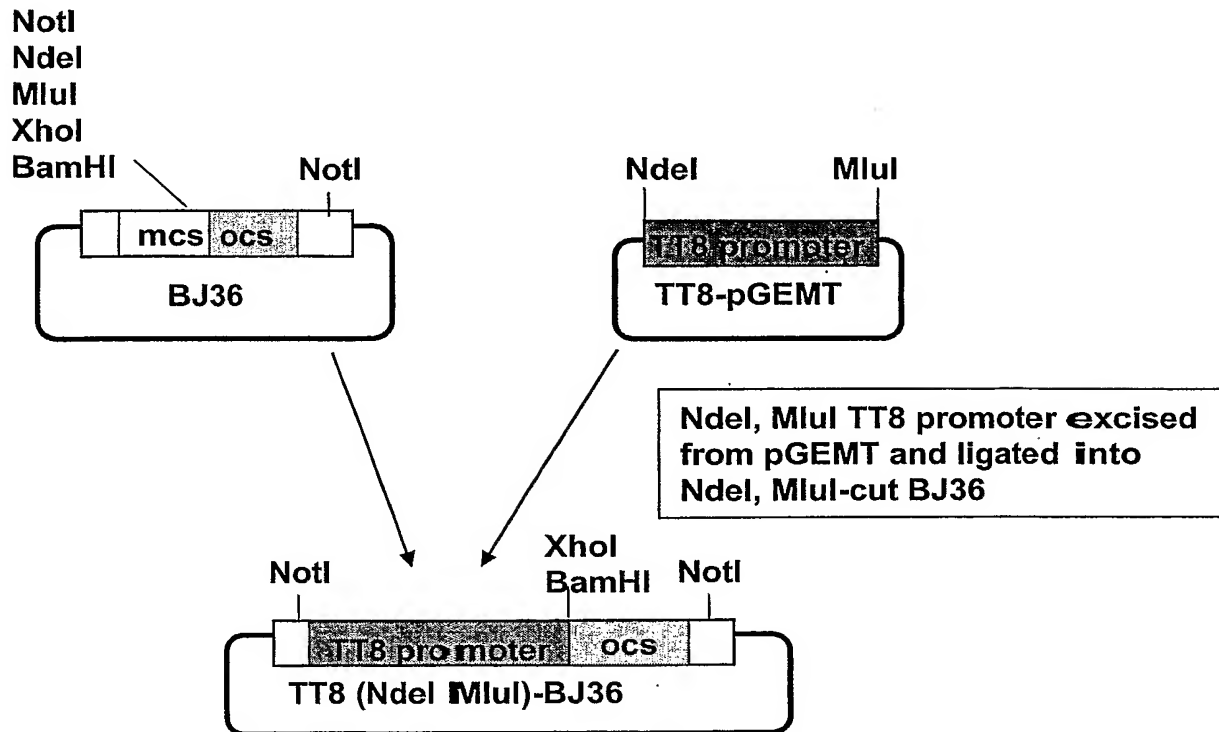
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**Example 10c(i)****Example 10c(ii)**

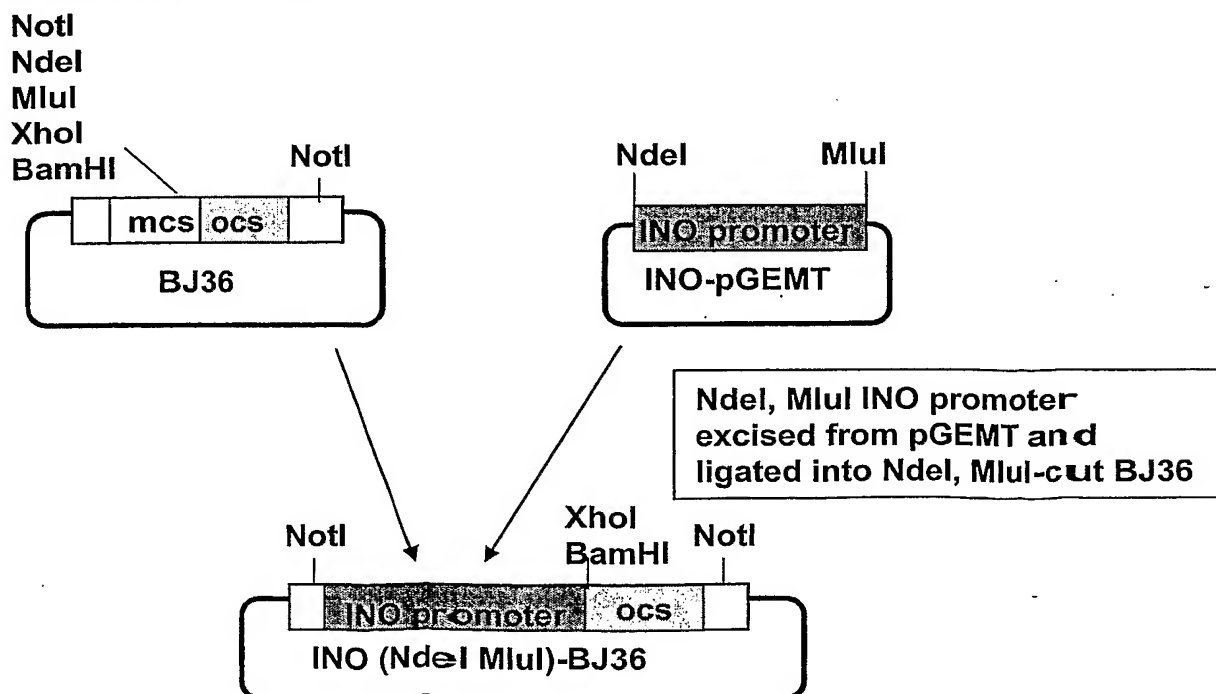
## Figure 19

### Cloning strategy, Example 11

#### Example 11a(i)

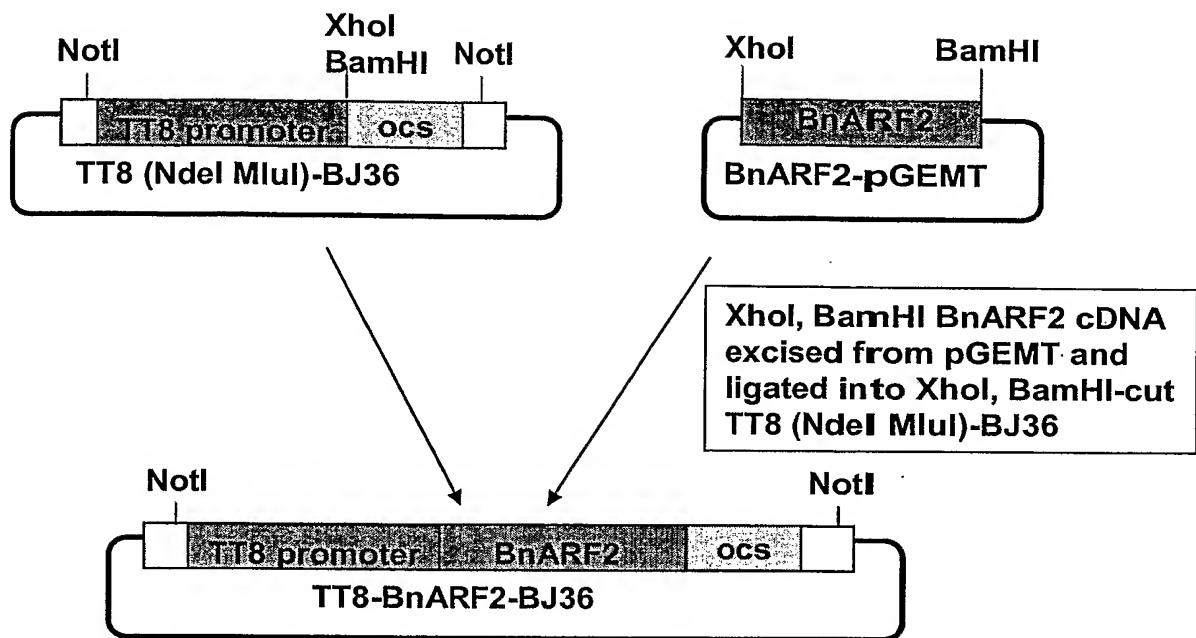
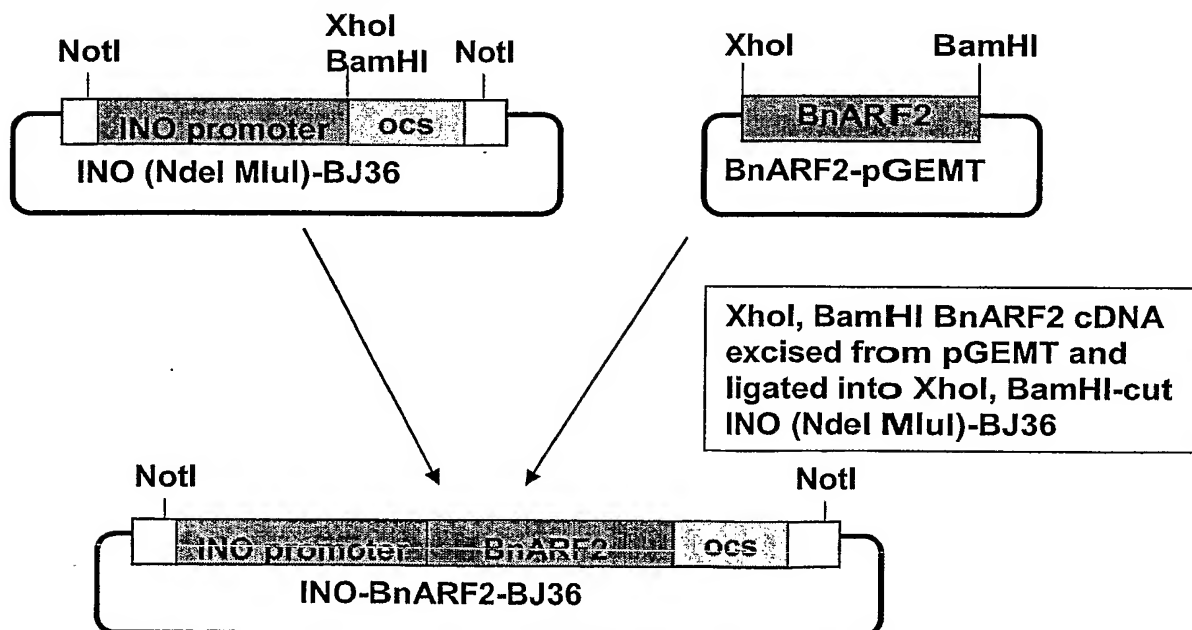


#### Example 11a(ii)

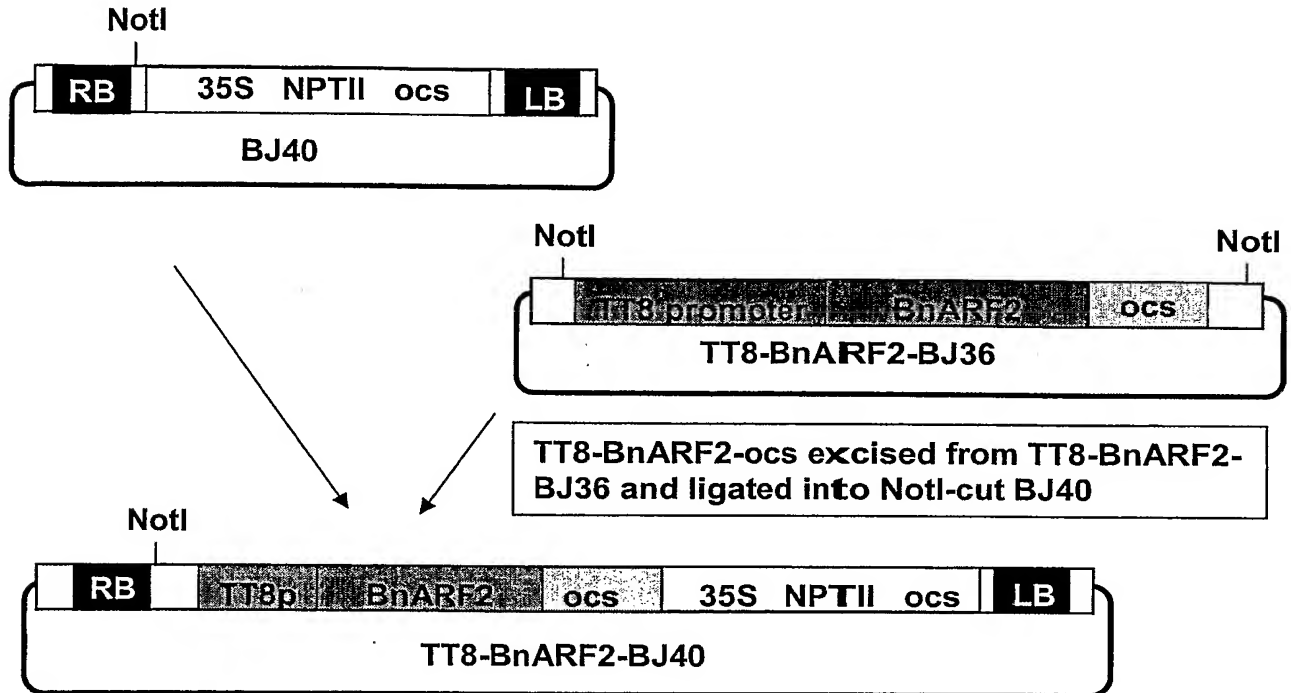
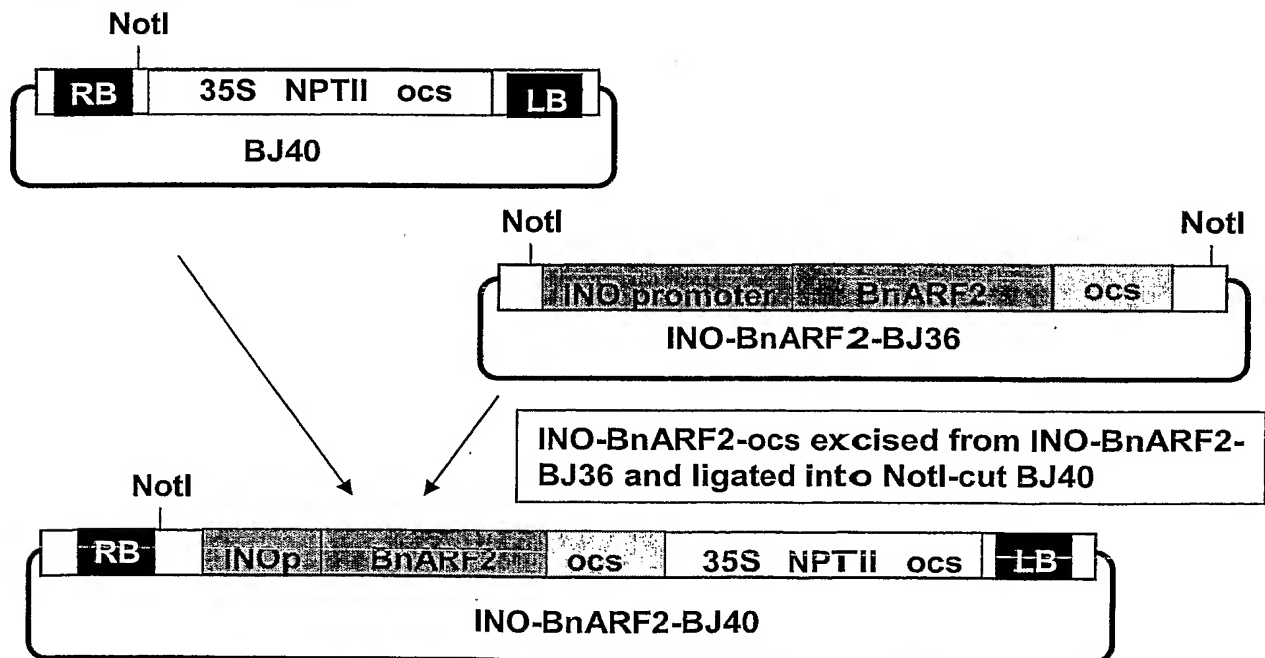




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**Example 11b(i)****Example 11b(ii)**

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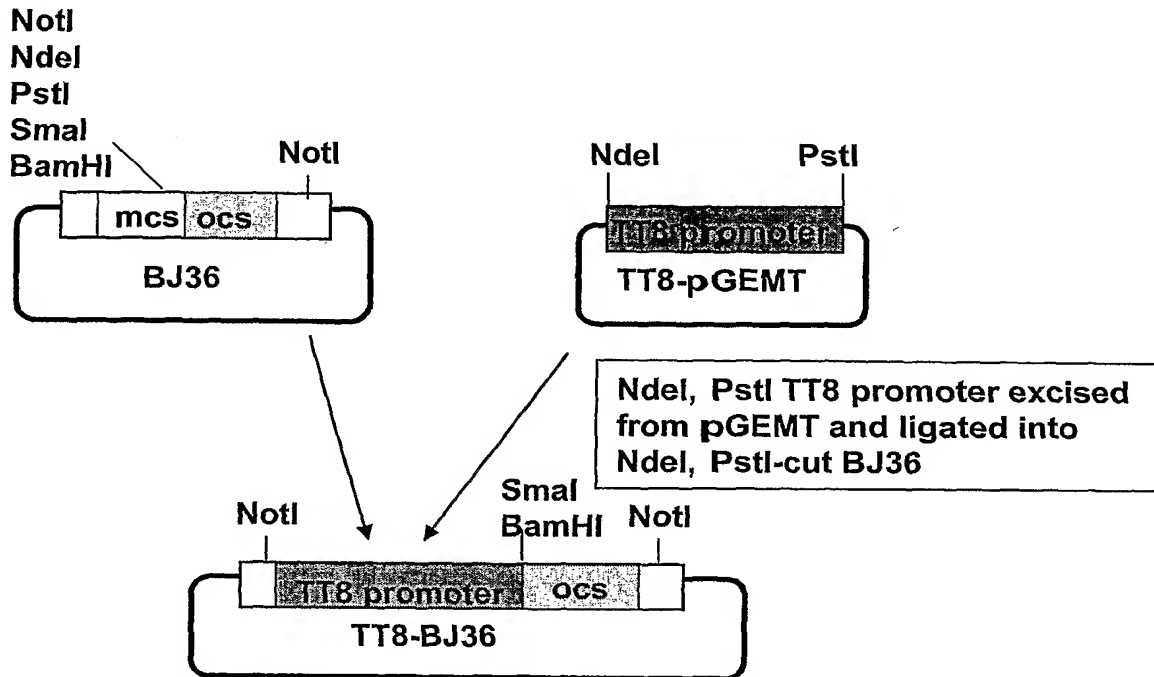
**Example 11c(i)****Example 11c(ii)**

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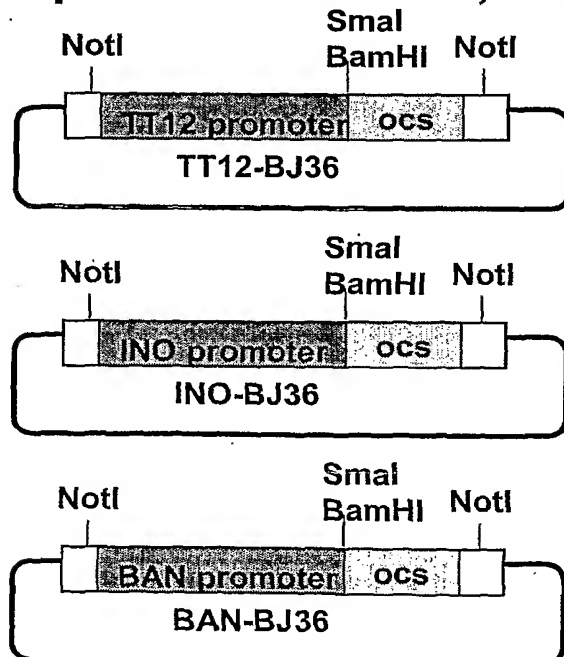
## Figure 20

### Cloning strategy, Examples 12, 13

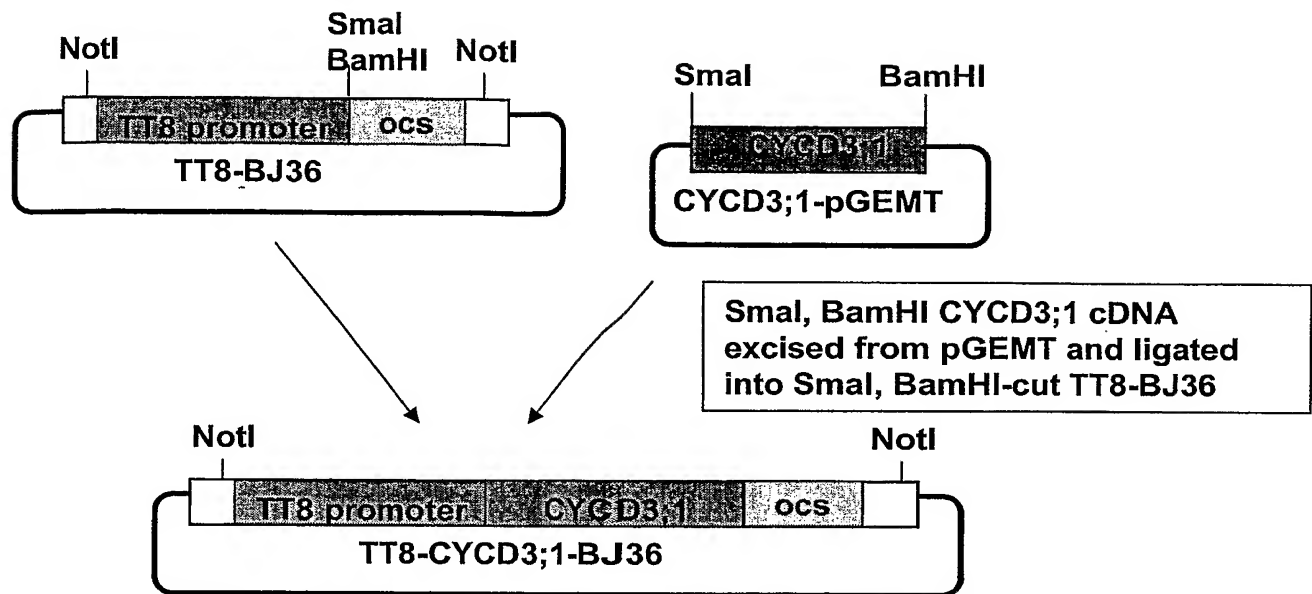
#### Examples 12a, 13a



Repeat process with TT12, INO, BAN promoters



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**Examples 12b, 13b**

**Repeat process with IPT1, ANT, CYCB1;1 cDNAs and TT12, INO, BAN promoters**

TT8-IPT1-BJ40

INO-CYCD3;1-BJ40

TT8-ANT-BJ40

INO-IPT1-BJ40

TT8-CYCB1;1-BJ40

INO-ANT-BJ40

TT12-CYCD3;1-BJ40

INO-CYCB1;1-BJ40

TT12-IPT1-BJ40

BAN-CYCD3;1-BJ40

TT12-ANT-BJ40

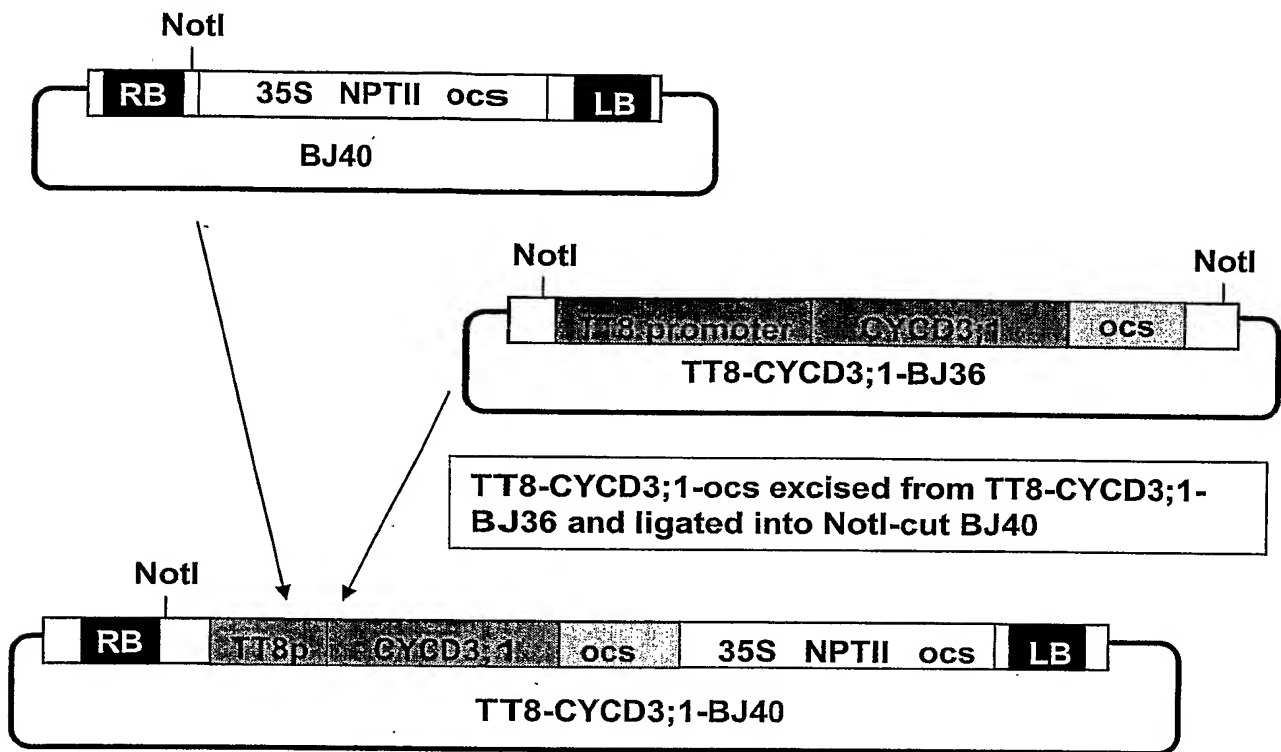
BAN-IPT1-BJ40

TT12-CYCB1;1-BJ40

BAN-ANT-BJ40

BAN-CYCB1;1-BJ40

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**Example 12c, 13c**

**Repeat process with all BJ36 constructs shown in Example 12b**

TT8-IPT1-BJ40

INO-CYCD3;1-BJ40

TT8-ANT-BJ40

INO-IPT1-BJ40

TT8-CYCB1;1-BJ40

INO-ANT-BJ40

TT12-CYCD3;1-BJ40

INO-CYCB1;1-BJ40

TT12-IPT1-BJ40

BAN-CYCD3;1-BJ40

TT12-ANT-BJ40

BAN-IPT1-BJ40

TT12-CYCB1;1-BJ40

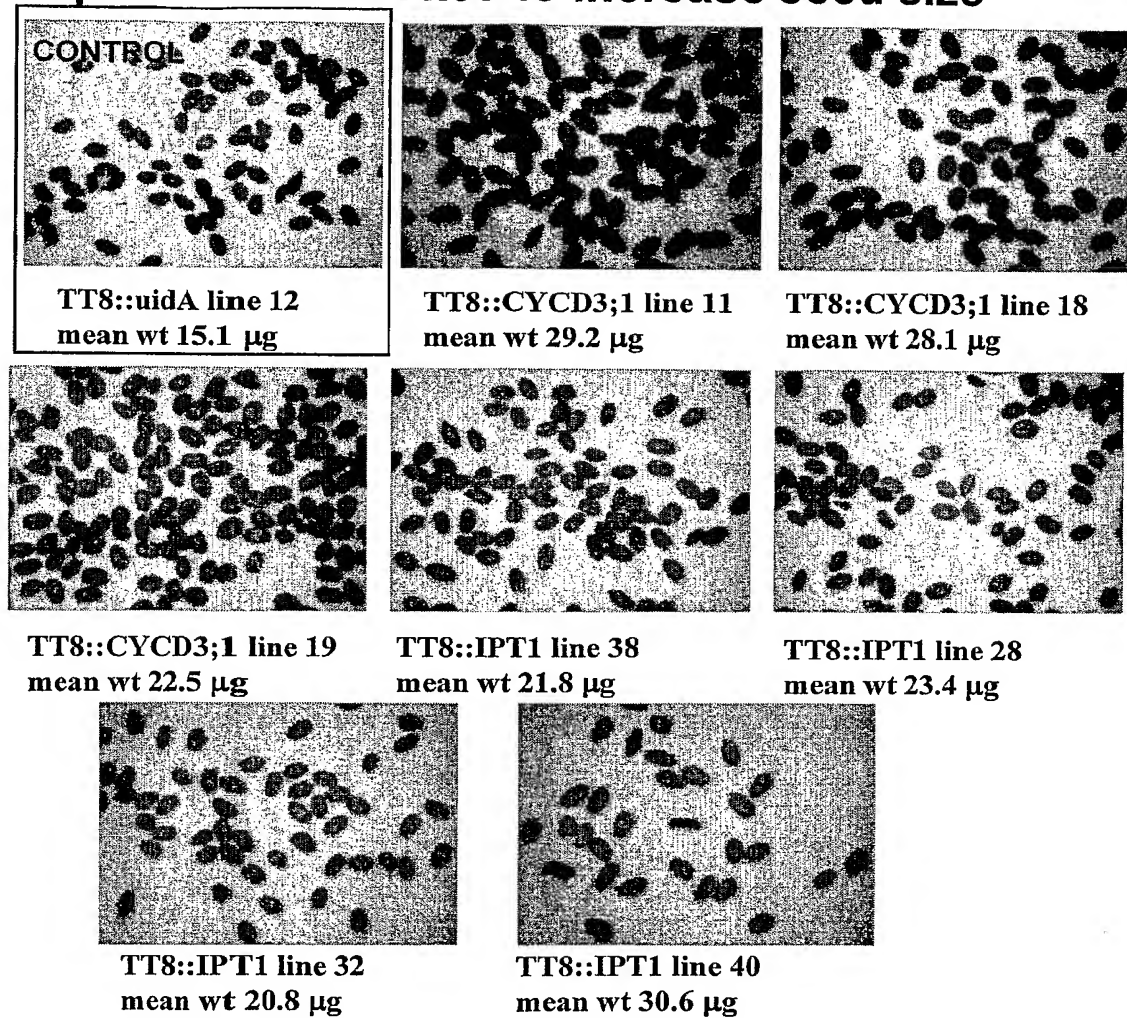
BAN-ANT-BJ40

BAN-CYCB1;1-BJ40

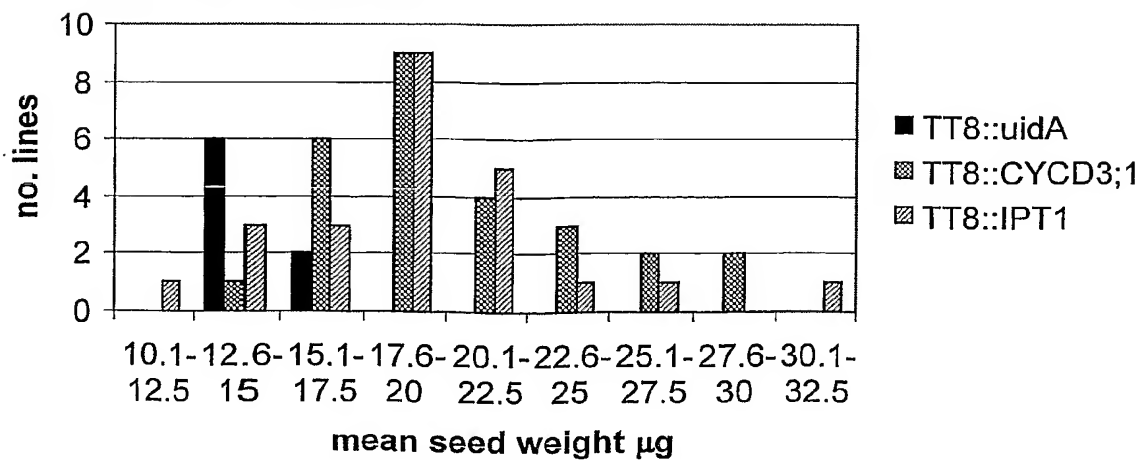
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## Figure 21A

### Expression cassettes to increase seed size



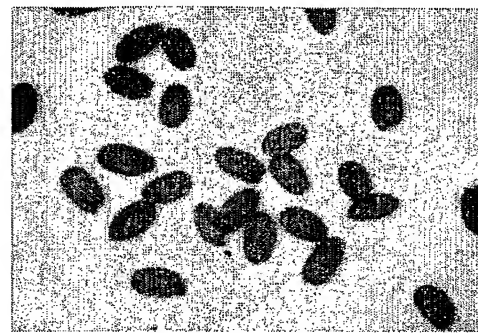
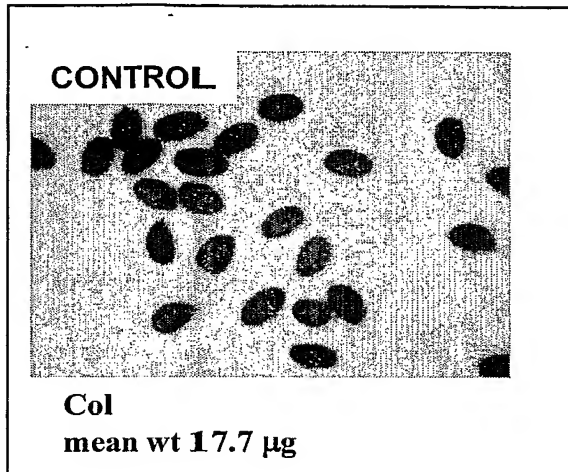
Distribution of seed weights in TT8::uidA (control), TT8::CYCD3;1, and TT8::IPT1 families



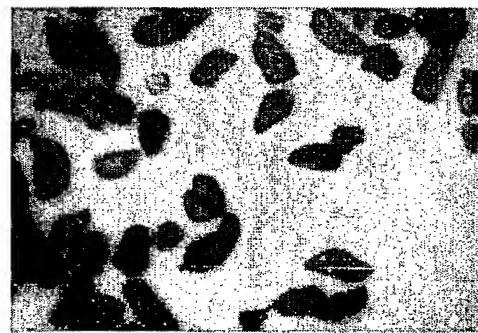
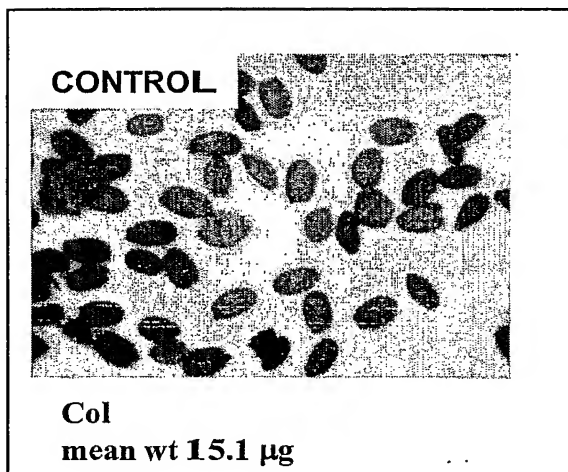
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## Figure 21B

Expression cassettes to increase seed size



**BAN::CYCD3;1 line 1**  
mean wt 23.9  $\mu$ g

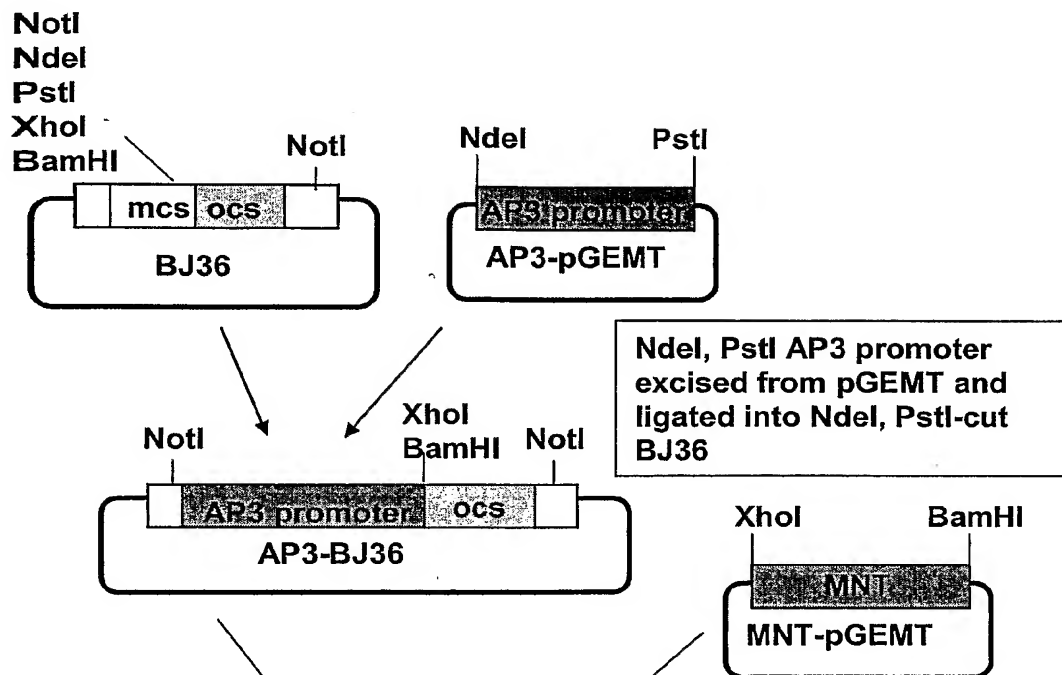


**INO::IPT1 line 9**  
mean wt 23.1  $\mu$ g

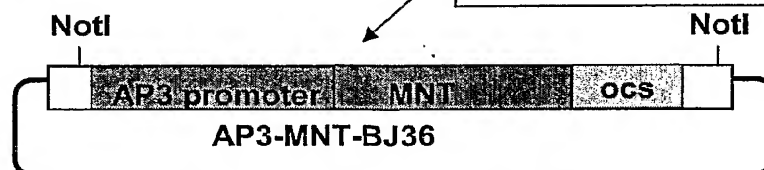
## Figure 22

### Cloning strategy, Example 14

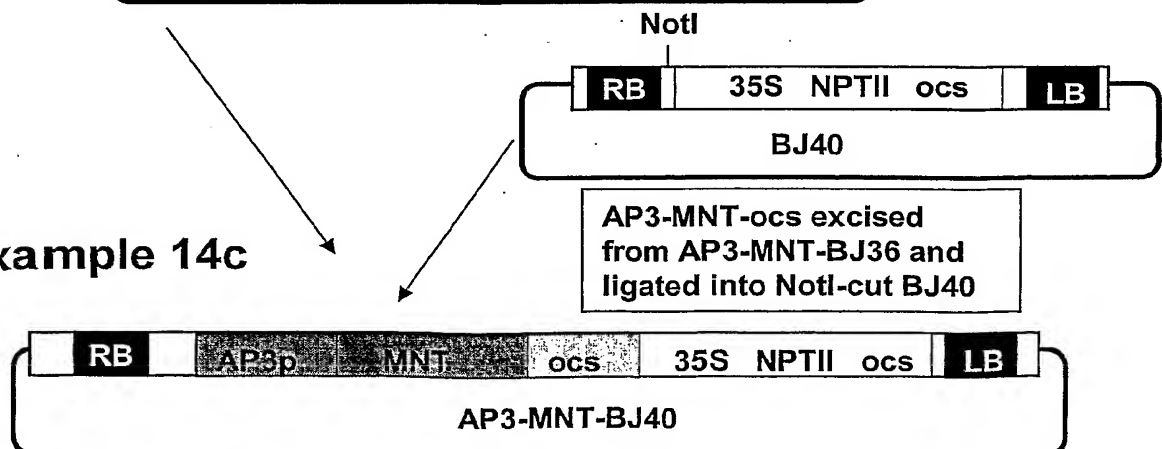
#### Example 14a



#### Example 14b



#### Example 14c

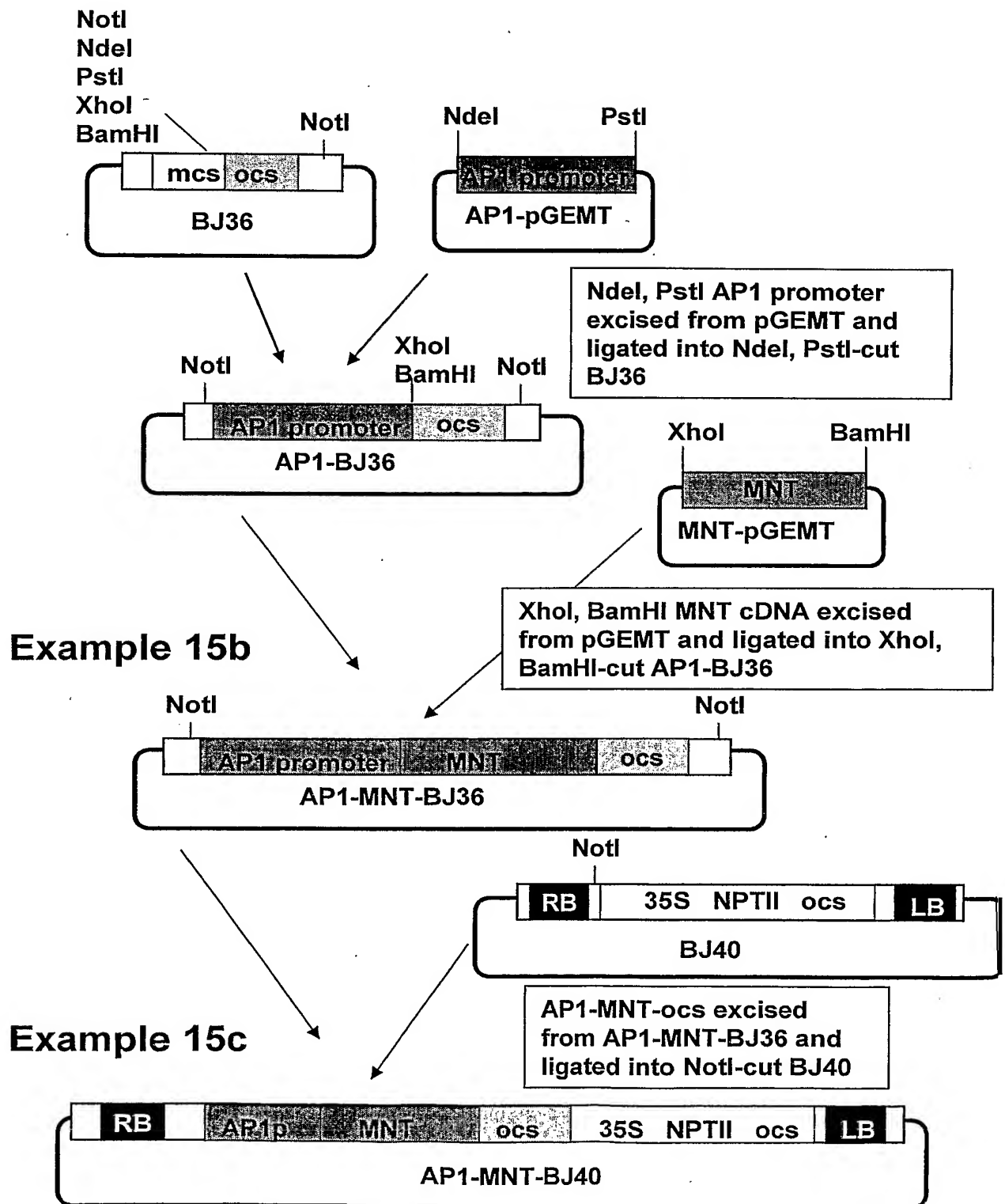




# Figure 23

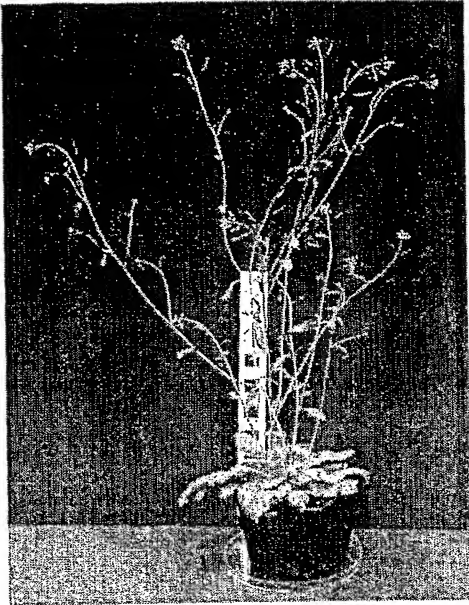
## Cloning strategy, Example 15

### Example 15a

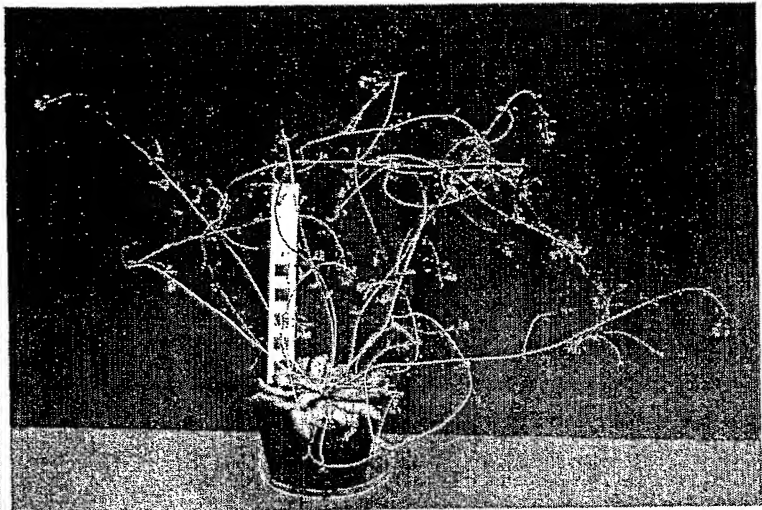


## Figure 24

### 24A Wild-type vs *mnt-1* plants



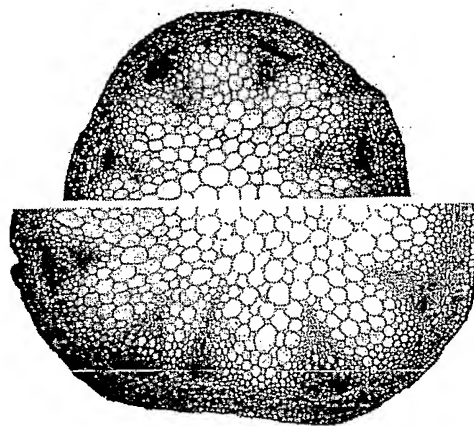
w.t.



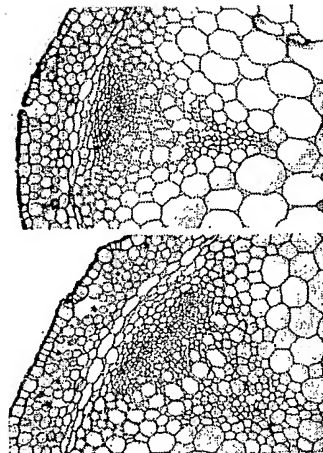
*mnt-1*

### 24B Wild-type vs *mnt-1* stems, transverse sections

w.t.



*mnt-1*



# Figure 25

## Cloning strategy, Example 18

### Example 18a

